STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 112948

TO: Celine Qian
Location: rem/2a89
Art Unit: 1636
Thursday, January 29, 2004

Case Serial Number: 09/780532

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

Search and Information Resources Administration

CRFE

Access DB# 112948

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 1/28/04

Art Unit: 1636 Phone Number: 2-0777 Serial Number: 09/780532

Mail Box and Bldg Room Location: Remsen 2A39 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need: 1/1 E

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Trade molecules and uses related thereto

Inventors (please provide full names): Clive Wood et al.

Earliest Priority Filing Date: 2/11/00

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search for SEQ ID NO:2 (both commercial and interference database)

417AA

STAFF USE ONLY

Searcher: 1/29/04

Searcher Phone #: 1/30/04

Type of Search

NA Sequence (#): ___

AA Sequence (#): 1

Vendors and cost where applicable

STN: ___

Dialog: ___ ABSS05P

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches
Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art **not found:***
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send compl t d forms to STIC/Biotech-Chem Library Remsen Bldg.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:32:31 ; Search time 46 Seconds
(without alignments)
1438.891 Million cell updates/sec

Title: US-09-780-532A-2
Perfect score: 2256
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....LDQESGAIIHPATQTSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2256	100.0	417	22	AAU04492	Human TRADE-alpha
2	2255	100.0	417	20	AAW98146	Human TRAIN-R. Ho
3	2255	100.0	417	21	AAB33474	Human PRO4333 prot
4	2255	100.0	417	22	AAU29260	Human PRO polypept
5	2255	100.0	417	22	AAB82412	Human tumour necro
6	2255	100.0	417	23	ABB95567	Human angiogenesis
7	2255	100.0	417	23	ABB84961	Human PRO4333 prot
8	2255	100.0	417	23	AAU83701	Human PRO protein,
9	2255	100.0	417	24	ABU71348	Human PRO4333 prot
10	2255	100.0	417	24	ABU65805	Human secreted/tra
11	2255	100.0	417	24	ABU66138	Novel human secret
12	2255	100.0	417	24	ABU67642	Human secreted/tra
13	2255	100.0	417	24	ABU65500	Human PRO polypept
14	2255	100.0	417	24	ABU58636	Human PRO polypept
15	2255	100.0	417	24	ABU56172	Human secreted/tra
16	2255	100.0	417	24	ABU57167	Human PRO polypept
17	2255	100.0	417	24	ABU10746	Human secreted/tra
18	2233	99.0	423	20	AAW85724	Novel protein (Clo
19	2233	99.0	423	22	AAU04493	Human TRADE-beta p
20	2231	98.9	417	19	AAW70386	Amino acid sequenc
21	2230	98.8	423	20	AAW93581	Human hAPO4-alpha
22	2230	98.8	423	21	AAB23547	Human Troy protein
23	2222	98.5	423	19	AAW70387	Amino acid sequenc
24	1567.5	69.5	416	21	AAB23546	Murine Troy protei
25	1567.5	69.5	416	22	AAU04494	Murine TRADE polyp
26	1565.5	69.4	416	20	AAW93579	Mouse mAPO4-alpha
27	1553.5	68.9	328	20	AAY06400	Human NTR-5 recept
28	973	43.1	214	20	AAY06522	Mouse STRIFE1 (Tan
29	973	43.1	214	20	AAW98145	Mouse TRAIN-R (lon
30	973	43.1	214	20	AAW93580	Mouse mAPO4-alpha
31	973	43.1	214	21	AAB23548	Murine dTroy prote
32	973	43.1	214	23	ABG78030	Human STRIFE1. Ho
33	865	38.3	210	20	AAY22223	Human TNFR superfa
34	865	38.3	210	21	AAB28555	Human TNFR soluble
35	857	38.0	150	20	AAW98148	TRAIN-R short, sol
36	783	34.7	160	20	AAY06399	Mouse NTR-5 recept
37	752	33.3	166	22	AAM24239	Human EST encoded
38	721	32.0	150	20	AAY06523	Mouse STRIFE2 (Tan
39	721	32.0	150	20	AAY22224	Mouse TNFR superfa
40	721	32.0	150	20	AAW98144	Mouse TRAIN-R (sho
41	721	32.0	150	20	AAW93583	Mouse mAPO4-gamma
42	721	32.0	150	21	AAB28556	Mouse TNFR soluble
43	721	32.0	150	21	AAY77465	Murine Rank-like p
44	721	32.0	150	23	ABG78031	Human STRIFE2. Ho
45	721	32.0	150	24	AAO26528	Mouse RANK-like pr

ALIGNMENTS

RESULT 1
AAU04492
ID AAU04492 standard; Protein; 417 AA.
XX
AC AAU04492;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human TRADE-alpha polypeptide.
XX
KW TRADE-alpha; TRADE-beta; proliferation; apoptosis; inflammation; liver;
KW NFkB signalling pathway; JNK signalling pathway; neoplasia; carcinoma;
KW necrosis; adenocarcinoma; lung; brain; intestine; Crohn's disease;
KW prostate; myelokathexis; autoimmune lymphoproliferative syndrome; human;
KW Alzheimer's disease; amyotrophic lateral sclerosis; epithelial cell.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..25
FT		/note= "Signal peptide"
FT	Domain	1..168
FT		/note= "Extracellular domain"
FT	Protein	26..417
FT		/note= "Mature TRADE-alpha protein"
FT	Domain	29..63
FT		/note= "Cysteine-rich domain #1"
FT	Domain	72..114
FT		/note= "Cysteine-rich domain #2"
FT	Modified-site	105..108
FT		/note= "Asn is N-glycosylated"
FT	Domain	114..139

```
FT                   /note= "Cysteine-rich domain #3"
FT   Domain          137..168
FT                   /note= "Serine/threonine/proline-rich domain"
FT   Domain          169..192
FT                   /note= "Transmembrane domain"
FT   Domain          193..417
FT                   /note= "Intracellular domain"
FT   Modified-site   200..203
FT                   /note= "Ser is phosphorylated by cAMP/cGMP-dependent
FT                          protein kinase"
FT   Modified-site   205..207
FT                   /note= "Ser is phosphorylated by protein kinase C"
FT   Modified-site   207..213
FT                   /note= "Tyrosine is phosphorylated by tyrosine kinase"
FT   Modified-site   215..220
FT                   /note= "Gly is N-myristoylated"
FT   Domain          218..417
FT                   /note= "TRADE-related death effector domain"
FT   Modified-site   219..222
FT                   /note= "Ser is phosphorylated by casein kinase II"
FT   Modified-site   238..241
FT                   /note= "Ser is phosphorylated by cAMP/cGMP-dependent
FT                          protein kinase"
FT   Modified-site   325..328
FT                   /note= "Ser is phosphorylated by casein kinase II"
XX
PN   WO200158954-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US04238.
XX
PR   11-FEB-2000; 2000US-0181922.
PR   14-FEB-2000; 2000US-0182148.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Wood C,  Chaudhary D,  Long A;
XX
DR   WPI; 2001-502708/55.
DR   N-PSDB; AAS08983.
XX
PT   Modulation of cell proliferation for the treatment of cancer comprises
PT   contacting a cell with a TRADE family peptide which modulates cell
PT   peptide activity or expression -
XX
PS   Disclosure; Fig 1; 173pp; English.
XX
CC   The sequence represents a human TRADE-alpha polypeptide. TRADE molecules
CC   are useful for the regulation of cellular processes such as cell
CC   proliferation (e.g., by inducing either proliferation or apoptosis), via
CC   the NFkB and JNK signalling pathways. A cell can be contacted with an
CC   agent that modulates the expression of a TRADE-alpha or TRADE-beta
CC   polypeptide, hence altering the rate of proliferation. Modulating agents
CC   may also be used in the detection of TRADE associated proliferative
CC   disorders such as inflammation, neoplasia, apoptosis or necrosis. The
CC   treatable neoplasia is a carcinoma or an adenocarcinoma present in
CC   epithelial cells e.g., of the lung, liver, brain, intestine or prostate.
CC   Other TRADE associated disorders include Crohn's disease, myelokathexis,
CC   autoimmune lymphoproliferative syndrome, Alzheimer's disease and
CC   amyotrophic lateral sclerosis.
XX
SQ   Sequence   417 AA;

  Query Match             100.0%;  Score 2256;  DB 22;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-192;
  Matches  417;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
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Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417


RESULT 2
AAW98146
ID   AAW98146 standard; Protein; 417 AA.
XX
AC   AAW98146;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human TRAIN-R.
XX
KW   TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /note= "signal peptide"
FT   Protein         22..417
FT                   /note= "mature protein"
FT   Domain          26..173
FT                   /note= "extracellular domain"
FT   Domain          174..190
FT                   /note= "transmembrane domain"
FT   Domain          191..417
FT                   /note= "cytoplasmic domain"
XX
PN   WO9913078-A1.
XX
PD   18-MAR-1999.
XX
PF   11-SEP-1998;   98WO-US19030.
XX
PR   06-MAY-1998;   98US-0084422.
PR   12-SEP-1997;   97US-0058631.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Hession C,  Tschopp J;
XX
DR   WPI; 1999-229238/19.
DR   N-PSDB; AAX24978.
XX
PT   New cysteine-rich tumor necrosis factor receptor
XX
PS   Claim 2; Page 26; 30pp; English.
XX
CC   The present sequence is a novel human cysteine-rich tumour
```

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CC   necrosis factor receptor family member termed TRAIN-R that is
CC   expressed at low levels in every tissue and cell line tested thus
CC   far, with higher expression detected in heart, prostate, ovary,
CC   testis, peripheral blood lymphocytes, thyroid and adrenal gland.
CC   Cell death can be induced by administering an agent capable of
CC   inhibiting the binding of TRAIN-R to its ligand.  A claimed method
CC   of treating, or reducing, the advancement, severity or effects of
CC   an immunological disease in a mammal comprises administering a
CC   pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC   e.g. soluble TRAIN-R.  TRAIN-R can be fused to an immunoglobulin to
CC   produce a fusion protein which may be targeted to various sites.
CC   It can be used in binding assays, and to identify antagonists and
CC   agonists.  Anti-TRAIN-R antibodies can be used to reduce the
CC   severity of an immune response or to treat cancer.  TRAIN-R
CC   blocking agents can also be used to reduce the severity or effects
CC   of an immunological disease (all claimed).
XX
SQ   Sequence   417 AA;

  Query Match             100.0%;  Score 2255;  DB 20;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-192;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
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Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||:||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 3
AAB33474
ID   AAB33474 standard; Protein; 417 AA.
XX
AC   AAB33474;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO4333 protein UNQ1888 SEQ ID NO:286.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58639.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 122; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
```

```
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   417 AA;

  Query Match             100.0%;  Score 2255;  DB 21;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-192;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 4
AAU29260
ID   AAU29260 standard; Protein; 417 AA.
XX
AC   AAU29260;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #237.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46161.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 11; Fig 474; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence   417 AA;

  Query Match             100.0%;  Score 2255;  DB 22;  Length 417;
```

```
  Best Local Similarity   99.8%;  Pred. No. 2.4e-192;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 5
AAB82412
ID AAB82412 standard; Protein; 417 AA.
XX
AC AAB82412;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human tumour necrosis factor receptor R248.
XX
KW Tumour necrosis factor receptor; R248; human; antiarthritic;
KW antirheumatic; antiasthmatic; antidiabetic; antiinflammatory.
KW asthma; rheumatoid arthritis; diabetes; inflammation; infection;
KW chronic obstructive pulmonary disease; nephritis; heart disease;
KW therapy.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..25
FT		/label= Signal_peptide
FT	Protein	26..417
FT		/label= Mature_protein
FT	Region	1..168
FT		/label= Extracellular region
FT	Region	169..192
FT		/label= Transmembrane region
FT	Region	193..417
FT		/label= Intracellular region
FT	Domain	31..72
FT		/label= CRD1
FT		/note= "cysteine-rich domain 1"
FT	Domain	75..114
FT		/label= CDR2
FT		/note= "cysteine-rich domain 2"
FT	Domain	117..149
FT		/label= CRD3
FT		/note= "cysteine-rich domain CDR3"
FT	Modified-site	105
FT		/note= "N-glycosylated"
FT	Binding-site	34..146
FT		/note= "predicted ligand binding site"

XX
PN WO200138526-A1.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-GB04438.
XX
PR 23-NOV-1999; 99GB-0027681.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Kitson JDA;
XX
DR WPI; 2001-367687/38.
DR N-PSDB; AAF90463.
XX
PT Novel isolated human tumour necrosis factor receptor polypeptide, R248,
PT or its variant capable of activating NF-kappaB useful for treating
PT asthma, rheumatoid arthritis, heart disease, nephritis, diabetes -
XX
PS Claim 1(i); Fig 1; 34pp; English.
XX
CC The present sequence is that of novel human tumour necrosis factor
CC receptor R248. R248 is expressed in activated lymphocytes but not
CC in resting lymphocytes, suggesting a role in chronic inflammatory
CC diseases, such as rheumatoid arthritis and asthma. Expression in
CC chondrocytes indicates a role in bone metabolism, which is important
CC in the bone destruction observed in rheumatoid arthritis,
CC osteoarthritis and steroid mediated bone erosion. Expression of the
CC receptor in epithelial cell layers in liver gut and pancreas
CC implicates R248 in inflammation associated with these tissues.
CC R248 is capable of activating NF-kappaB. cDNA (see AAF90463)
CC encoding R248 was obtained by PCR amplification of human aortic
CC smooth muscle cell cDNA using R248-specific primers. R248 is a
CC screening target for the identification of novel pharmaceutical
CC agents which modulate the activity of the receptor, or which
CC modulate activation of NF-kappaB by the receptor. Such agents are
CC used in a claimed method of treating a subject having an immune or
CC inflammatory disorder or smooth muscle cell disorder, such as
CC asthma, rheumatoid arthritis, chronic obstructive pulmonary disease,
CC diabetes, inflammation associated with bacterial or viral infection,
CC nephritis and heart disease.
XX
SQ Sequence 417 AA;

```
  Query Match             100.0%;  Score 2255;  DB 22;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-192;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
```

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Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 6
ABB95567
ID ABB95567 standard; Protein; 417 AA.
XX
AC ABB95567;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO4333 SEQ ID NO: 290.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95705.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 290; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 23; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 7
ABB84961
ID ABB84961 standard; Protein; 417 AA.
XX
AC ABB84961;

XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO4333 protein sequence SEQ ID NO:290.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88216.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 290; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 23; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
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Db   61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy  121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
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Db  121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy  181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
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Db  181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy  241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy  301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy  361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
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Db  361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 8
AAU83701
ID AAU83701 standard; Protein; 417 AA.
XX
AC AAU83701;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 220.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX

PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABK33645.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 220; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 23; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 9
ABU71348
ID ABU71348 standard; Protein; 417 AA.
XX
AC ABU71348;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO4333 protein.
XX
KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
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PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
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PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.

PR 18-SEP-1997; 97US-059263P.
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PR 01-JUL-1998; 98US-091359P.
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PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
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PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
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PR 26-AUG-1998; 98US-097974P.
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PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
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PR 10-SEP-1998; 98US-099763P.
PR 10-SEP-1998; 98US-099812P.

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  Query Match             100.0%;  Score 2255;  DB 24;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-192;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
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Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
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Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 10
ABU65805
ID   ABU65805 standard; Protein; 417 AA.
XX
AC   ABU65805;
XX
DT   19-MAY-2003  (first entry)
XX
DE   Human secreted/transmembrane protein, SEQ ID 474.
XX
KW   Human; PRO; secreted protein; transmembrane protein;
KW   cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW   colon tumour; breast tumour; prostate tumour; rectal tumour;
KW   cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW   tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW   cartilage disorder; sports injury.
XX
OS   Homo sapiens.
XX
PN   US2003036156-A1.
XX
PD   20-FEB-2003.
XX
PF   02-JUL-2002; 2002US-0188767.
XX
PR   16-SEP-1998;   98WO-US19330.
PR   07-OCT-1998;   98WO-US21141.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28551.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
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Best Local Similarity 99.8%; Pred. No. 2.4e-192;
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RESULT 11
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KW gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003036157-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188769.
XX

PR 16-SEP-1998; 98WO-US19330.
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RESULT 12
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XX
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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PF 12-JUL-2002; 2002US-0194423.
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PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
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PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
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PR 22-MAY-2000; 2000WO-US14042.
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PR 28-JUL-2000; 2000WO-US20710.
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PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
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PR 26-JUN-1998; 98US-0105413.
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PR 07-DEC-1998; 98US-0202054.
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PR 22-MAR-2001; 2001US-0816744.
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PR 25-MAY-2001; 2001US-0866028.
PR 05-JUN-2001; 2001US-0874503.

PR 18-JUL-2001; 2001US-0908827.
PR 30-JUL-2001; 2001US-0918585.
PR 06-AUG-2001; 2001US-0924419.
PR 13-AUG-2001; 2001US-0929404.
PR 16-AUG-2001; 2001US-0931836.
PR 28-AUG-2001; 2001US-0941992.
PR 04-SEP-2001; 2001US-0946374.
PR 15-JAN-2002; 2002US-0052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J; Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332039/31.
DR N-PSDB; ACA05936.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids,
PT useful in gene therapy, in chromosome and gene mapping, as chromosome
PT markers, in tissue typing, and in chromosome identification -
XX
PS Claim 11; Fig 474; 706pp; English.
XX
CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ABU67406-ABU67710 are the PRO polypeptides of the invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 24; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

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Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
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Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 13
ABU65500
ID ABU65500 standard; Protein; 417 AA.
XX
AC ABU65500;
XX
DT 16-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #237.
XX
KW Human; PRO; cytostatic; chromosome mapping; gene mapping;
KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
KW chondrocyte differentiation; chondrocyte proliferation; tumour.
XX
OS Homo sapiens.
XX
PN US2003032102-A1.
XX
PD 13-FEB-2003.
XX
PF 17-JUN-2002; 2002US-0173697.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
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PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
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PR 20-DEC-2000; 2000WO-US34956.
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Query Match 100.0%; Score 2255; DB 24; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
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Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
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Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
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Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
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Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
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Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 14
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ID   ABU58636 standard; Protein; 417 AA.
XX
AC   ABU58636;
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DT   15-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #237.
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KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach;
KW   liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027272-A1.
XX
PD   06-FEB-2003.
XX
PF   21-JUN-2002; 2002US-0176492.
XX
PR   16-SEP-1998;   98WO-US19330.
PR   07-OCT-1998;   98WO-US21141.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99WO-US05190.
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PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
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PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28551.
PR   30-DEC-1999;   99WO-US31274.
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PR   15-MAR-2000; 2000WO-US06884.
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GenCore version 5.1.6

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Listing first 45 summaries

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SUMMARIES

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2	710.5	31.5	151	3	US-09-286-529-4	Sequence 4, Appli
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25	133.5	5.9	197	4	US-09-000-166-1	Sequence 1, Appli
26	133	5.9	625	3	US-08-996-139-15	Sequence 15, Appl
27	133	5.9	625	3	US-08-995-659-15	Sequence 15, Appl
28	133	5.9	625	3	US-09-215-649A-15	Sequence 15, Appl
29	133	5.9	625	4	US-09-577-780-15	Sequence 15, Appl
30	133	5.9	625	4	US-09-577-800-15	Sequence 15, Appl
31	133	5.9	625	4	US-09-466-496-15	Sequence 15, Appl
32	133	5.9	625	4	US-09-871-856-15	Sequence 15, Appl
33	133	5.9	625	4	US-09-871-291-15	Sequence 15, Appl
34	132.5	5.9	2050	2	US-08-347-594A-2	Sequence 2, Appli
35	132.5	5.9	2813	4	US-09-381-261A-1	Sequence 1, Appli
36	132	5.9	176	3	US-09-411-722-1	Sequence 1, Appli
37	132	5.9	276	3	US-09-041-886-27	Sequence 27, Appl
38	132	5.9	277	3	US-09-042-785A-10	Sequence 10, Appl
39	132	5.9	277	3	US-09-006-353A-10	Sequence 10, Appl
40	132	5.9	277	4	US-08-114-944D-2	Sequence 2, Appli
41	132	5.9	277	4	US-09-573-986-10	Sequence 10, Appl
42	132	5.9	277	4	US-08-338-975A-2	Sequence 2, Appli
43	131	5.8	139	2	US-08-219-237B-8	Sequence 8, Appli
44	131	5.8	355	1	US-08-292-549-6	Sequence 6, Appli
45	131	5.8	355	3	US-09-006-353A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-286-529-3
; Sequence 3, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 210
; TYPE: PRT
; ORGANISM: human
US-09-286-529-3

Query Match 38.3%; Score 865; DB 3; Length 210;
Best Local Similarity 83.2%; Pred. No. 7.6e-73;
Matches 153; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

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Qy       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
           |||||        |  :: | :|:|||:||:||||||||:||||||| | ||||||||||
Db       1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60

Qy      61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
           |||||||||||| || |||||||||||||| |||:|||||:|||| ||||:|||||||
Db      61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120

Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
           |||||||||||||||||||||||||||||| ||||||||:|| |||||||:||||||||||
Db     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTAVAAVICSALAT 180

Qy     181 VLLA 184
           ||||
Db     181 VLLA 184
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RESULT 2
US-09-286-529-4
; Sequence 4, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25

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;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: human
US-09-286-529-4

  Query Match             31.5%;  Score 710.5;  DB 3;  Length 151;
  Best Local Similarity   81.3%;  Pred. No. 1.2e-58;
  Matches  122;  Conservative   10;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDC-RQQEFRDRSGNCVPCNQCGPGMELS 59
              ||||||       |  ::  | :|:|||:||:||| |||||:|||||||.| |||||||||
Db          1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCSRQQEFKDRSGNCVLCKQCGPGMELS 60

Qy         60 KECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLP 119
              ||||||||||||| || |||||||||||||| |||:|||||:|||| ||||:||||||
Db         61 KECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLP 120

Qy        120 GFYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
              ||||||||||||||||||||||||||||||
Db        121 GFYRKTKLVGFQDMECVPCGDPPPPYEPHC 150


RESULT 3
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Pan, James
;  APPLICANT: Yan, Minhong
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1739R1
;  CURRENT APPLICATION NUMBER: US/09/548,130
;  CURRENT FILING DATE: 2000-04-12
;  EARLIER APPLICATION NUMBER: US 60/128,849
;  EARLIER FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
;   LENGTH: 297
;   TYPE: PRT
;   ORGANISM: Human
US-09-548-130-6

  Query Match             21.3%;  Score 480.5;  DB 4;  Length 297;
  Best Local Similarity   39.7%;  Pred. No. 8.7e-37;
  Matches   91;  Conservative   34;  Mismatches   97;  Indels    7;  Gaps    1;

Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |: |: | || | :|||| ||||:||:| | || |   |   |:|  ||  :|: |
Db          2 DCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQSC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| || ||:|||:|:|||||| ||||||:: | || ||:||    |  |  || :
Db         62 ITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQ 212
              ::||:  :    |::  | |:: | |    || | |  :|||: |       |   :
Db        122 LSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEAD 181

Qy        213 YNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACS 261
                | | |  |   | :  :         |   |:        |: ||
Db        182 KTAKEESLFPVPPSKETSAESQVSENIFQTQPLNPI-------LEDDCS 223


RESULT 4
US-09-548-130-3
; Sequence 3, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Pan, James
;  APPLICANT: Yan, Minhong
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1739R1
;  CURRENT APPLICATION NUMBER: US/09/548,130
;  CURRENT FILING DATE: 2000-04-12
;  EARLIER APPLICATION NUMBER: US 60/128,849
;  EARLIER FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Human
US-09-548-130-3

  Query Match             21.2%;  Score 477.5;  DB 4;  Length 299;
  Best Local Similarity   39.4%;  Pred. No. 1.7e-36;
  Matches   91;  Conservative   37;  Mismatches   94;  Indels    9;  Gaps    2;

Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |: |: | || | :|||| ||||:||:| | || |   |   |:|  ||  :|: |
Db          2 DCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQSC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| || ||:|||:|:|||||| ||||||:: | || ||:||    |  |  || :
Db         62 ITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFME--KKPSWSLRSQD 210
              ::||:  :    |::  | |:: | |    || | |  :|||: |    :: :  |   :
Db        122 LSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRVTGGLLQFE 181

Qy        211 IQYNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACS 261
                | | |  |   | :  :         |   |:        |: ||
Db        182 ADKTAKEESLFPVPPSKETSAESQVSENIFQTQPLNPI-------LEDDCS 225


RESULT 5
US-09-342-681C-17
; Sequence 17, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
;  APPLICANT: Zonana et al.
;  TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
;  FILE REFERENCE: 52978
;  CURRENT APPLICATION NUMBER: US/09/342,681C
;  CURRENT FILING DATE:  1999-06-29
;  PRIOR APPLICATION NUMBER: 60/092,279
;  PRIOR FILING DATE: 1998-07-09
;  PRIOR APPLICATION NUMBER: 60/112,366
;  PRIOR FILING DATE: 1998-12-15
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-342-681C-17

  Query Match              8.5%;  Score 191;  DB 4;  Length 448;
  Best Local Similarity   28.7%;  Pred. No. 1.5e-09;
  Matches   62;  Conservative   30;  Mismatches   84;  Indels   40;  Gaps   12;

Qy         16 LLVLLGYLSCKVTCESGDCRQQEFRDR-SGNCVPCNQCGPGMELSKECGFG-YGEDAQCV 73
              | ||:  | |    |  :| : |: :: :| |  |  ||||  |    ||:|   ||  ||
Db         13 LPVLVVSLMCSARAEYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCGYGTKDEDYGCV 72

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANC----SATSDAICGDCLPGFY----RKT 125
                 |   :| :  |:| |:   ||      | :|          :|| || ||||:|    |
Db         73 PCPAEKFSKG-GYQICRRHKDC---EGFFRATVLTPGDMENDAECGPCLPGYYMLENRPR 128

Qy        126 KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKI------ASTASSPRDTA---------L 170
               : |   | |  |    ||    |    :           |:  ||   |         |
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```
Db        129 NIYG---MVCYSC-LLAPPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKELSGQGHL 184

Qy        171 AAVICSALATVL---LALLILCVIYCKRQFMEKKPS 203
              |  :  |::|:    :|:::: : |     :: |||
Db        185 ATALIIAMSTIFIMAIAIVLIIMFY----ILKTKPS 216


RESULT 6
US-09-342-681C-19
; Sequence 19, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
;  APPLICANT: Zonana et al.
;  TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
;  FILE REFERENCE: 52978
;  CURRENT APPLICATION NUMBER: US/09/342,681C
;  CURRENT FILING DATE:  1999-06-29
;  PRIOR APPLICATION NUMBER: 60/092,279
;  PRIOR FILING DATE: 1998-07-09
;  PRIOR APPLICATION NUMBER: 60/112,366
;  PRIOR FILING DATE: 1998-12-15
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-342-681C-19

  Query Match             8.5%;  Score 191;  DB 4;  Length 448;
  Best Local Similarity   28.7%;  Pred. No. 1.5e-09;
  Matches   62;  Conservative   30;  Mismatches   84;  Indels   40;  Gaps   12;

Qy         16 LLVLLGYLSCKVTCESGDCRQQEFRDR-SGNCVPCNQCGPGMELSKECGFG-YGEDAQCV 73
              | ||:  | |     |  :| : |: :: :| |  |  ||||  |    ||:|   ||  ||
Db         13 LPVLVVSLMCSARAEYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCGYGTKDEDYGCV 72

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANC----SATSDAICGDCLPGFY----RKT 125
                |   :| :  |:| |:   ||     | :|          :|| || ||||:|    |
Db         73 PCPAEKFSKG-GYQICRRHKDC---EGFFRATVLTPGDMENDAECGPCLPGYYMLENRPR 128

Qy        126 KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKI------ASTASSPRDTA---------L 170
              : |   | |  |    ||    |    :          |:  ||   |          |
Db        129 NIYG---MVCYSC-LLAPPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKELSGQGHL 184

Qy        171 AAVICSALATVL---LALLILCVIYCKRQFMEKKPS 203
              |  :  |::|:    :|:::: : |     :: |||
Db        185 ATALIIAMSTIFIMAIAIVLIIMFY----ILKTKPS 216


RESULT 7
US-08-097-827-11
; Sequence 11, Application US/08097827
;   GENERAL INFORMATION:
;        APPLICANT: Baum, Peter
;                   Goodwin, Ray
;                   Fanslow, William
;                   Gayle, Richard
;        TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
;                            OX40
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Immunex Corporation
;             STREET: 51 University Street
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98101
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/097,827
;             FILING DATE: 23-Jul-1993
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Perkins, Patricia A.
;             REGISTRATION NUMBER: 34,693
;             REFERENCE/DOCKET NUMBER: 2806
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-587-0730
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 438 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

  Query Match             7.0%;  Score 159;  DB 1;  Length 438;
  Best Local Similarity   27.5%;  Pred. No. 1.4e-06;
  Matches   69;  Conservative   31;  Mismatches   93;  Indels   58;  Gaps   18;

Qy         15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
              | |:||| |:  ||     :| :  :    ||: |  | :| ||  :   |   :  |  |
Db          9 TALLLLG-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVNRC--DHTRDTLCH 61

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
                |    : |   :  || |  |   :  : | ||: | | :|  | ||   :      ||
Db         62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy        133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
                   ::||||  ||  : |     |    |           |   :| || |   | ||
Db        115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy        180 TVLLALLILCVIYCKRQFMEKKPSW---SLRSQDIQYNGSELSCFDRPQLHEYAHRACCQ 236
              |:|               :  ::|::   :::|  :    |||     | | |   |:|
Db        172 TLL-------------WETQRPTFRPTTVQSTTVWPRTSELP--STPTLVE--PRSC-- 211

Qy        237 CRRDSVQTCGP 247
                |   || |
Db        212 ---DKTHTCPP 219


RESULT 8
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
;  GENERAL INFORMATION:
;    APPLICANT:  Baum, Peter
;    APPLICANT:  Goodwin, Ray
;    APPLICANT:  Fanslow, William
;    APPLICANT:  Gayle, Richard
;    TITLE OF INVENTION:  No. 5783665el Cytokine Which is a Ligand for
;    TITLE OF INVENTION:  OX40
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/494,574
;      FILING DATE:  22-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/097,827
;      FILING DATE:  23-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2806
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-587-0730
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  438 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-494-574-11

  Query Match             7.0%;  Score 159;  DB 1;  Length 438;
  Best Local Similarity   27.5%;  Pred. No. 1.4e-06;
  Matches   69;  Conservative   31;  Mismatches   93;  Indels   58;  Gaps   18;

Qy         15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
                | |:||| |:  ||    :| :  :   ||: |  | :| || :   |   :  | |
Db          9 TALLLLG-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVNRC--DHTRDTLCH 61

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
               |    : |   :  || |  |   :  : | ||: | | :|  | ||   :       ||
Db         62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy        133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
                   ::||||  ||  : |     |    |          |   :| || |   | ||
Db        115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy        180 TVLLALLILCVIYCKRQFMEKKPSW---SLRSQDIQYNGSELSCFDRPQLHEYAHRACCQ 236
              |:|                :  ::|::   :::|  :    |||     | | |   |:|
Db        172 TLL-------------WETQRPTFRPTTVQSTTVWPRTSELP--STPTLVE--PRSC-- 211

Qy        237 CRRDSVQTCGP 247
                  |   || |
Db        212 ---DKTHTCPP 219


RESULT 9
US-08-097-827-7
; Sequence 7, Application US/08097827
;   GENERAL INFORMATION:
;        APPLICANT: Baum, Peter
;                   Goodwin, Ray
;                   Fanslow, William
;                   Gayle, Richard
;        TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
;                            OX40
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Immunex Corporation
;             STREET: 51 University Street
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98101
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/097,827
;             FILING DATE: 23-Jul-1993
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Perkins, Patricia A.
;             REGISTRATION NUMBER: 34,693
;             REFERENCE/DOCKET NUMBER: 2806
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-587-0730
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 206 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-097-827-7

  Query Match             6.6%;  Score 150;  DB 1;  Length 206;
  Best Local Similarity   30.1%;  Pred. No. 3.5e-06;
  Matches   55;  Conservative   21;  Mismatches   75;  Indels   32;  Gaps   13;

Qy         15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
                | |:||| |:  ||    :| :  :   ||: |  | :| || :   |   :  | |
Db          9 TALLLLG-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVNRC--DHTRDTLCH 61

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
               |    : |   :  || |  |   :  : | ||: | | :|  | ||   :       ||
Db         62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy        133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
                   ::||||  ||  : |     |    |          |   :| || |   | ||
Db        115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy        180 TVL 182
              |:|
Db        172 TLL 174


RESULT 10
US-08-494-574-7
; Sequence 7, Application US/08494574
; Patent No. 5783665
;  GENERAL INFORMATION:
;    APPLICANT:  Baum, Peter
;    APPLICANT:  Goodwin, Ray
;    APPLICANT:  Fanslow, William
;    APPLICANT:  Gayle, Richard
;    TITLE OF INVENTION:  No. 5783665el Cytokine Which is a Ligand for
;    TITLE OF INVENTION:  OX40
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/494,574
;      FILING DATE:  22-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/097,827
;      FILING DATE:  23-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2806
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-587-0730
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  206 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-08-494-574-7

  Query Match              6.6%;  Score 150;  DB 1;  Length 206;
  Best Local Similarity   30.1%;  Pred. No. 3.5e-06;
  Matches   55;  Conservative   21;  Mismatches   75;  Indels   32;  Gaps   13;

Qy         15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
              | |:||| |:  ||    :| :  :   ||: |  | :| ||  :   |   :  | |
Db          9 TALLLLG-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVNRC--DHTRDTLCH 61

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
               |    : |   :  || |  |   :  : | ||: | | :|  | ||   :       ||
Db         62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy        133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
                   ::||||  ||  : |     |    |           |   :| || |   | ||
Db        115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy        180 TVL 182
              |:|
Db        172 TLL 174


RESULT 11
US-08-974-022-51
; Sequence 51, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  205 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-51

  Query Match              6.4%;  Score 145;  DB 3;  Length 205;
  Best Local Similarity   29.8%;  Pred. No. 1e-05;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
                :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
               :        ::||||  ||  : |     |    |       :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
              |   | |||:|
Db        163 CEDRSLLATLL 173


RESULT 12
US-08-795-445A-51
; Sequence 51, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  205 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-445A-51

  Query Match              6.4%;  Score 145;  DB 3;  Length 205;
  Best Local Similarity   29.8%;  Pred. No. 1e-05;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
                :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
               :        ::||||  ||  : |     |    |       :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
```

```
                    |   | |||:|
Db        163 CEDRSLLATLL 173


RESULT 13
US-08-795-447A-51
; Sequence 51, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  205 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-447A-51

  Query Match             6.4%;  Score 145;  DB 3;  Length 205;
  Best Local Similarity   29.8%;  Pred. No. 1e-05;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
               :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
               :        ::|||| ||  : |     |     |      :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
               |   | |||:|
Db        163 CEDRSLLATLL 173


RESULT 14
US-08-974-186-51
; Sequence 51, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  205 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-186-51

  Query Match             6.4%;  Score 145;  DB 3;  Length 205;
  Best Local Similarity   29.8%;  Pred. No. 1e-05;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
               :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
               :        ::|||| ||  : |     |     |      :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
               |   | |||:|
Db        163 CEDRSLLATLL 173


RESULT 15
US-08-795-446B-51
; Sequence 51, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  205 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-446B-51

  Query Match             6.4%;  Score 145;  DB 3;  Length 205;
  Best Local Similarity   29.8%;  Pred. No. 1e-05;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
                :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
               :        ::||||  ||  : |     |    |      :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
              |   | |||:|
Db        163 CEDRSLLATLL 173

Search completed: January 29, 2004, 21:33:01
Job time : 21 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:32:01 ; Search time 40 Seconds
(without alignments)
2166.566 Million cell updates/sec

Title: US-09-780-532A-2
Perfect score: 2256
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....LDQESGAIIHPATQTSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2256	100.0	417	9	US-09-780-532-2	Sequence 2, Appli
2	2255	100.0	417	12	US-10-199-672-474	Sequence 474, App
3	2255	100.0	417	12	US-10-216-163-220	Sequence 220, App
4	2255	100.0	417	12	US-10-187-749-474	Sequence 474, App
5	2255	100.0	417	12	US-10-194-457-474	Sequence 474, App
6	2255	100.0	417	12	US-10-184-642-474	Sequence 474, App
7	2255	100.0	417	12	US-10-196-747-474	Sequence 474, App
8	2255	100.0	417	12	US-10-173-689-474	Sequence 474, App
9	2255	100.0	417	12	US-10-173-690-474	Sequence 474, App
10	2255	100.0	417	12	US-10-173-691-474	Sequence 474, App
11	2255	100.0	417	12	US-10-173-692-474	Sequence 474, App
12	2255	100.0	417	12	US-10-173-694-474	Sequence 474, App
13	2255	100.0	417	12	US-10-173-698-474	Sequence 474, App
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15	2255	100.0	417	12	US-10-173-707-474	Sequence 474, App
16	2255	100.0	417	12	US-10-174-569-474	Sequence 474, App
17	2255	100.0	417	12	US-10-174-583-474	Sequence 474, App
18	2255	100.0	417	12	US-10-174-587-474	Sequence 474, App
19	2255	100.0	417	12	US-10-174-589-474	Sequence 474, App
20	2255	100.0	417	12	US-10-174-591-474	Sequence 474, App
21	2255	100.0	417	12	US-10-175-736-474	Sequence 474, App
22	2255	100.0	417	12	US-10-175-742-474	Sequence 474, App
23	2255	100.0	417	12	US-10-175-744-474	Sequence 474, App
24	2255	100.0	417	12	US-10-175-745-474	Sequence 474, App
25	2255	100.0	417	12	US-10-175-748-474	Sequence 474, App
26	2255	100.0	417	12	US-10-175-751-474	Sequence 474, App
27	2255	100.0	417	12	US-10-175-754-474	Sequence 474, App
28	2255	100.0	417	12	US-10-176-480-474	Sequence 474, App
29	2255	100.0	417	12	US-10-176-489-474	Sequence 474, App
30	2255	100.0	417	12	US-10-176-754-474	Sequence 474, App
31	2255	100.0	417	12	US-10-176-755-474	Sequence 474, App
32	2255	100.0	417	12	US-10-176-759-474	Sequence 474, App
33	2255	100.0	417	12	US-10-176-920-474	Sequence 474, App
34	2255	100.0	417	12	US-10-176-922-474	Sequence 474, App
35	2255	100.0	417	12	US-10-176-924-474	Sequence 474, App
36	2255	100.0	417	12	US-10-176-984-474	Sequence 474, App
37	2255	100.0	417	12	US-10-179-508-474	Sequence 474, App
38	2255	100.0	417	12	US-10-179-512-474	Sequence 474, App
39	2255	100.0	417	12	US-10-179-515-474	Sequence 474, App
40	2255	100.0	417	12	US-10-173-702-474	Sequence 474, App
41	2255	100.0	417	12	US-10-173-703-474	Sequence 474, App
42	2255	100.0	417	12	US-10-173-704-474	Sequence 474, App
43	2255	100.0	417	12	US-10-174-574-474	Sequence 474, App
44	2255	100.0	417	12	US-10-176-486-474	Sequence 474, App
45	2255	100.0	417	12	US-10-176-490-474	Sequence 474, App

ALIGNMENTS

RESULT 1
US-09-780-532-2
; Sequence 2, Application US/09780532
; Patent No. US20020068696A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive
; APPLICANT: Chaudhary, Divya
; APPLICANT: Long, Andrew
; TITLE OF INVENTION: TRADE MOLECULES, AND USES RELATED THERETO
; FILE REFERENCE: GNN-012CP
; CURRENT APPLICATION NUMBER: US/09/780,532
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,922
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/182,148
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-532-2

Query Match 100.0%; Score 2256; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.8e-197;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
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RESULT 2
US-10-199-672-474
; Sequence 474, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 3
US-10-216-163-220
; Sequence 220, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 220
; LENGTH: 417

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;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-216-163-220

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 4
US-10-187-749-474
; Sequence 474, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/187,749
;  CURRENT FILING DATE:  2002-07-01
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-187-749-474

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 5
US-10-194-457-474
; Sequence 474, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C296
;  CURRENT APPLICATION NUMBER: US/10/194,457
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
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;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-194-457-474

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 6
US-10-184-642-474
; Sequence 474, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C194
;  CURRENT APPLICATION NUMBER: US/10/184,642
;  CURRENT FILING DATE:  2002-06-27
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-184-642-474

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 7
US-10-196-747-474
; Sequence 474, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C346
;  CURRENT APPLICATION NUMBER: US/10/196,747
;  CURRENT FILING DATE:  2002-07-16
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-196-747-474
```

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 8
US-10-173-689-474
; Sequence 474, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-689-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 9
US-10-173-690-474
; Sequence 474, Application US/10173690
; Publication No. US20030166105A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C9
; CURRENT APPLICATION NUMBER: US/10/173,690
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-690-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 10
US-10-173-691-474
; Sequence 474, Application US/10173691
; Publication No. US20030166106A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C13
;  CURRENT APPLICATION NUMBER: US/10/173,691
;  CURRENT FILING DATE:  2002-06-17
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-173-691-474

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 11
US-10-173-692-474
; Sequence 474, Application US/10173692
; Publication No. US20030166188A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C20
;  CURRENT APPLICATION NUMBER: US/10/173,692
;  CURRENT FILING DATE:  2002-06-17
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-173-692-474

  Query Match             100.0%;  Score 2255;  DB 12;  Length 417;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-197;
  Matches  416;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417


RESULT 12
US-10-173-694-474
; Sequence 474, Application US/10173694
; Publication No. US20030166107A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
```

; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C19
; CURRENT APPLICATION NUMBER: US/10/173,694
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-694-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
```

RESULT 13
US-10-173-698-474
; Sequence 474, Application US/10173698
; Publication No. US20030166108A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C12
; CURRENT APPLICATION NUMBER: US/10/173,698
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-698-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 14
US-10-173-699-474
; Sequence 474, Application US/10173699
; Publication No. US20030166109A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C8
; CURRENT APPLICATION NUMBER: US/10/173,699
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-699-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA 417
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RESULT 15
US-10-173-707-474
; Sequence 474, Application US/10173707
; Publication No. US20030166110A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C17
; CURRENT APPLICATION NUMBER: US/10/173,707
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-707-474

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:36:52 ; Search time 20 Seconds
(without alignments)
2005.117 Million cell updates/sec

Title: US-09-780-532A-2
Perfect score: 2256
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....LDQESGAIIHPATQTSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	157	7.0	454	1	GQMST1	tumor necrosis fac
2	148	6.6	416	1	JN0006	nerve growth facto
3	146.5	6.5	435	2	I54182	tumor necrosis fac
4	145	6.4	271	2	S12783	OX40 antigen precu
5	144	6.4	272	2	I48700	gene ox40 protein
6	143	6.3	1797	2	A55677	laminin beta-2 cha
7	142.5	6.3	1801	1	MMRTS	laminin beta-2 cha
8	142	6.3	1104	2	I38869	transcription fact
9	141.5	6.3	461	1	GQRTT1	tumor necrosis fac
10	135	6.0	425	1	A26431	nerve growth facto
11	133	5.9	1650	2	S53457	dominant autoantig
12	133	5.9	4660	2	T42737	gp330 protein prec
13	132.5	5.9	2813	1	VWHU	von Willebrand fac
14	132	5.9	277	2	A60771	B-cell activation
15	132	5.9	1786	1	MMMSB1	laminin beta-1 cha
16	130.5	5.8	1170	2	A40558	thrombospondin 1 p
17	129	5.7	326	1	GQVZML	T2 protein - myxom
18	126.5	5.6	1170	1	TSHUP1	thrombospondin 1 p
19	125.5	5.6	1798	2	S53869	laminin beta-2 cha
20	125	5.5	349	2	D72175	G2R protein - vari
21	124.5	5.5	1193	2	A44018	laminin B2t chain
22	124	5.5	837	2	S43656	furin (EC 3.4.21.7
23	124	5.5	1192	2	S69000	laminin gamma 2 ch
24	124	5.5	1299	2	T43251	furin (EC 3.4.21.7
25	123.5	5.5	965	2	S62935	hypothetical prote
26	123	5.5	256	2	B32393	T-cell antigen 4-1
27	123	5.5	1827	2	T34288	hypothetical prote
28	122.5	5.4	1548	2	S34583	serine proteinase
29	122	5.4	349	2	D36858	gene G4R protein -
30	122	5.4	1680	2	A43434	furin (EC 3.4.21.7
31	121.5	5.4	863	1	S51789	VLDL receptor prec
32	121	5.4	348	2	T28623	hypothetical prote
33	121	5.4	1786	1	MMHUB1	laminin beta-1 cha
34	121	5.4	1964	2	T09059	notch4 - mouse
35	119.5	5.3	3712	2	S18253	laminin alpha-1 ch
36	118.5	5.3	3075	2	S14458	laminin alpha-1 ch
37	118	5.2	255	2	I38426	lymphocyte activat
38	118	5.2	1106	2	T13938	gene shuttle craft
39	117.5	5.2	1119	2	A88481	protein C16A3.6 [i
40	116.5	5.2	493	2	JC5486	membrane glycoprot
41	116	5.1	1790	1	MMFFB1	laminin beta-1 cha
42	114.5	5.1	455	1	GQHUT1	tumor necrosis fac
43	114.5	5.1	557	2	A48434	variant-specific s
44	114.5	5.1	4753	1	A47437	LDL-receptor-relat
45	114	5.1	327	2	A46484	apoptosis-mediatin

ALIGNMENTS

RESULT 1
GQMST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldma
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell l
A;Reference number: I54532; MUID:94245292; PMID:8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: I57826; MUID:93156721; PMID:8381516

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A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.0%;  Score 157;  DB 1;  Length 454;
  Best Local Similarity   21.0%;  Pred. No. 0.00027;
  Matches   76;  Conservative   42;  Mismatches  140;  Indels  104;  Gaps   19;

Qy         34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGF-QKCKPC 92
              | | ::     | : | :|  |  |  :|    | | |  |     :  ::|  |
Db         44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCP-SPGRDTVCRECEKGTFTASQNYLRQCLSC 102

Qy         93 LDC-AVVNRFQKANCSATSDAICG-----------------DCLPGFYRKTKL------ 127
                |   ::: : : | |  | :||                 || | |     :
Db        103 KTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKETQ 162

Qy        128 -------VGF--QDMECVPCGDPPPPYEPHCASKVNLVKIA-----STASSPRDTALAAV 173
                    ||  :: |||||          ||      :|:      :  ::|:|:  | :
Db        163 NTVCNCHAGFFLRESECVPCS--------HCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214

Qy        174 ICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRA 233
              :      :|| | :|  |:     | : | |                    ||:::
Db        215 L---PLVILLGLCLLSFIFI--SLMCRYPRW-----------------RPEVYSII--- 248

Qy        234 CCQCRRDSV----QTCG-PVRLLPSMCCEEACSPNPATLGCGVHSAASLQARN------- 281
                | || |    :  | |:   ||         || |||     :|  :
Db        249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSPTSGFNP-TLGFSTPGFSSPVSSTPISPIFG 303

Qy        282 ------AGPAGEMVPTFFGS--LTQSICG----EFSDAWPLMQNPMGGDNISFCDSYPEL 329
                   |  |:|||      | :|:|          |    :|   ||      |  :
Db        304 PSNWHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWEDSAHPQRPDNADLAILYAVV 363

Qy        330 TG 331
               |
Db        364 DG 365


RESULT 2
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in t
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
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F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.6%;  Score 148;  DB 1;  Length 416;
  Best Local Similarity   31.0%;  Pred. No. 0.0012;
  Matches   58;  Conservative   17;  Mismatches   80;  Indels   32;  Gaps   11;

Qy         20 LGYLSCKVTC-ESGD----CRQQEFRDR-SGNCVPCNQCGPGMELSKECGFGY------G 67
              :|  |    | || |    |   |:|  ||:|  |: |        | |||
Db         82 VGLHSMSAPCVESDDAVCRCAYGYFQDELSGSCKECSIC--------EVGFGLMFPCRDS 133

Qy         68 EDAQCVTCRLHRFKEDWGFQKCKPCLDCAVV--NRFQKANCSATSDAICGDCLPGFYRKT 125
              :|  |  |    | ::  |    |||  | :   |      |:|||||  |  |  | :   |
Db        134 QDTVCEECPEGTFSDEANF--VDPCLPCTICEENEVMVKECTATSDAECRDLHPRWTTHT 191

Qy        126 -KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSP---RDTA--LAAVICSALA 179
               | |   |  |   |   |   :  ::|     :| |   | ||  |  | || ||
Db        192 PSLAGSDSPE--PITRDPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPVYCSILA 249

Qy        180 TVLLALL 186
                |:: |:
Db        250 AVVVGLV 256


RESULT 3
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

  Query Match             6.5%;  Score 146.5;  DB 2;  Length 435;
  Best Local Similarity   21.4%;  Pred. No. 0.0016;
  Matches   73;  Conservative   42;  Mismatches  107;  Indels  119;  Gaps   19;

Qy         16 LLVLLGYLSCK-------VTCESGDCRQQE---FRDRSGNCVPCNQCGPGMELSKECGFG 65
              :| | | |:           |:  || ||    :  :    |  |::| ||  :| :|
Db         18 VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQHRIC--CSRCPPGTYVSAKC--S 73

Qy         66 YGEDAQCVTCRLHRFKEDWGF----QKCKPC------LDCAVVNRFQKANCSATSDAIC- 114
```

```
Db        74 RIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA 133

Qy       115 ------------GDCLPGFYRKTK-LVGFQDMECVPC--------GDPPPPYEPH--CAS 151
Db       134 AWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCEN 193

Qy       152 KVNLVKIA-------STASSPRD--------TALAAVICSALATVLLALLILCVIY---- 192
Db       194 Q-GLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLMLAVLLPLAFFLLLATVFSCIWKSHP 252

Qy       193 --CKR--QFMEKKP----------SWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCR 238
Db       253 SLCRKLGSLLKRRPQGEGPNPVAGSW----------------EPPKAHPYF-------- 287

Qy       239 RDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQA 279
Db       288 PDLVQPLLPI-----------SGDVSPVSTGLPAAPVLEA 316
```

RESULT 4
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match 6.4%; Score 145; DB 2; Length 271;
  Best Local Similarity 29.8%; Pred. No. 0.0012;
  Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;

```
Qy         9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
Db         6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy        64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
Db        52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy       123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
Db       110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy       175 C---SALATVL 182
Db       163 CEDRSLLATLL 173
```

RESULT 5
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match 6.4%; Score 144; DB 2; Length 272;
  Best Local Similarity 29.5%; Pred. No. 0.0015;
  Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;

```
Qy        15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
Db         9 TALLLLA-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVSRC--DHTRDTLCH 61

Qy        74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
Db        62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy       133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
Db       115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy       180 TVL 182
Db       172 TLL 174
```

RESULT 6
A55677
laminin beta-2 chain precursor (version 1) - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C;Accession: A55677
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A;Reference number: A55677; MUID:95213013; PMID:7698745
A;Accession: A55677
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1797 <WEW>
A;Cross-references: GB:X79683
C;Genetics:
A;Gene: GDB:LAMB2
A;Cross-references: GDB:132363; OMIM:150325
A;Map position: 3p21.3-3p21.2
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F;283-344/Domain: laminin-type EGF-like homology <LE01>
F;347-407/Domain: laminin-type EGF-like homology <LE02>
F;410-467/Domain: laminin-type EGF-like homology <LE03>
F;470-519/Domain: laminin-type EGF-like homology <LE04>
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;783-828/Domain: laminin-type EGF-like homology <LE06>
F;831-874/Domain: laminin-type EGF-like homology <LE07>
F;877-924/Domain: laminin-type EGF-like homology <LE08>
F;927-982/Domain: laminin-type EGF-like homology <LE09>
F;985-1034/Domain: laminin-type EGF-like homology <LE10>
```
```

F;1037-1091/Domain: laminin-type EGF-like homology <LE11>
F;1094-1139/Domain: laminin-type EGF-like homology <LE12>
F;1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.3%; Score 143; DB 2; Length 1797;
Best Local Similarity 22.1%; Pred. No. 0.013;
Matches 87; Conservative 35; Mismatches 145; Indels 126; Gaps 24;

```
Qy        17 LVLLGYLSCKVTCESGDCRQQEFRDRSGNCV--------PCNQCGPGMELSKECGFGYG- 67
Db       775 LIYNGALPCQ--CNPQGSLSSECNPHGGQCLCKPGVVGRRCDTCAPGY-------YGFGP 825

Qy        68 --------------------EDAQCVTCRLHRF--------KEDWGFQKCKPCL------ 93
Db       826 TGCQACQCSPRGALSSLCERTSGQCL-CRTGAFGLRCDACQRGQWGFPSCRPCVCNGHAD 884

Qy        94 DCAVVNRFQKA--NC-SATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPP-PPYEPHC 149
Db       885 EC---NTHTGACLGCRDLTGGEHCERCIAGFHGDPRLP--YGAQCRPCPCPEGPGSQRHF 939

Qy       150 ASKVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFME-KKP------ 202
Db       940 AT-----------SCHQDEYSQQIVCHCRAGY---TGLRCEACAPGQFGDPSRPGACQLC 985

Qy       203 --SWSLRSQDIQ----YNGSELSCF----------DRPQLHEYA-----HRACCQCRRDS 241
Db       986 ECSGNIDPMDPDACDPHPGQCLRCLHHTEGPHCAHSKPGFHGQAARQSCHRCTCNLLGTN 1045

Qy       242 VQTC------------GPVRLLPSM--CCEEACSPN--PATLGCGVHSAASLQARNAGP- 284
Db      1046 PQQCPSPDQCHCDPSSGQCPCLPNVQALAVDRCAPNFWNLTSGHGCQPCACLPSREEGPT 1105

Qy       285 ----AGEMVP-TFFGSLTQSICGEFSDAWPLMQ 312
Db      1106 CNEFTGQCHPGAGFGGRTCSECQELHWGDPGLQ 1138
```

RESULT 7
MMRTS
laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurc
A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539
A;Molecule type: mRNA
A;Residues: 1-1801 <HUN>
A;Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F;36-285/Domain: VI <DOM6>
F;286-555/Domain: V <DOM5>
F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;556-784/Domain: IV <DOM4>
F;786-831/Domain: laminin-type EGF-like homology <LE06>
F;788-1196/Domain: III <DOM3>
F;834-877/Domain: laminin-type EGF-like homology <LE07>
F;880-927/Domain: laminin-type EGF-like homology <LE08>
F;930-986/Domain: laminin-type EGF-like homology <LE09>
F;989-1038/Domain: laminin-type EGF-like homology <LE10>

F;1041-1095/Domain: laminin-type EGF-like homology <LE11>
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1>
F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.3%; Score 142.5; DB 1; Length 1801;
Best Local Similarity 22.6%; Pred. No. 0.015;
Matches 98; Conservative 33; Mismatches 147; Indels 155; Gaps 27;

```
Qy        17 LVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKEC--------GFG--- 65
Db       778 LVYNGALPCQ--CDPQGSLSSECNPHGGQC----RCKPGV-VGRRCDACATGYYGFGPAG 830

Qy        66 ----------------YGEDAQCVTCRLHRF--------KEDWGFQKCKPCLDCAVVNRF 101
Db       831 CQACQCSPDGALSALCEGTSGQCL-CRTGAFGLRCDHCQRGQWGFPNCRPC-----VCNG 884

Qy       102 QKANCSATSDAI-----------CGDCLPGFYRKTKL-VGFQDMECVPCGDPP-PPYEPH 148
Db       885 RADECDAHTGACLGCRDYTGGEHCERCIAGFHGDPRLPYGGQ---CRPCPCPEGPGSQRH 941

Qy       149 CASKVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFME-KKPSWSLR 207
Db       942 FAT-----------SCHRDGYSQQIVCHCRAGY---TGLRCEACAPGHFGDPSKPGGRCQ 987

Qy       208 ----SQDIQ---------YNGSELSCFD----------RPQLHEYA-----HRACCQCRR 239
Db       988 LCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCKPGFHGQAARQSCHRCTCNLLG 1047

Qy       240 DSVQTC------------GPVRLLP---SMCCEEACSPN--PATLGCGVHSAASLQARNA 282
Db      1048 TDPQRCPSTDLCHCDPSTGQCPCLPHVQGLSCDR-CAPNFWNFTSGRGCQPCACHPSRAR 1106

Qy       283 GP------------AGEMVPTFFGSLTQSICGEFSDAWPLMQ------NPMGGD------ 318
Db      1107 GPTCNEFTGQCHCHAG------FGGRTCSECQELHWGDPGLQCRACDCDPRGIDKPQCHR 1160

Qy       319 NISFCDSYPELTG 331
Db      1161 STGHCSCRPGVSG 1173
```

RESULT 8
I38869
transcription factor NFX1 [imported] - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
C;Accession: I38869
R;Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.
J. Exp. Med. 180, 1763-1774, 1994
A;Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the
n and functions as a transcriptional repressor.
A;Reference number: I38869; MUID:95053707; PMID:7964459
A;Accession: I38869
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1104 <RES>
A;Cross-references: EMBL:U15306; NID:g563216; PIDN:AAA69517.1; PID:g563217
C;Superfamily: RING finger homology
F;338-398/Domain: RING finger homology <RRN>

Query Match 6.3%; Score 142; DB 2; Length 1104;
Best Local Similarity 18.8%; Pred. No. 0.0094;
Matches 110; Conservative 58; Mismatches 182; Indels 236; Gaps 27;

```
Qy        24 SCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG-------FGYGEDAQC---- 72
```

```
Db        440 SCNLLCHPG--------------PCPPCPAFMTKTCECGRTRHTVRCGQAVSVHCSNPC 484

Qy         73 ---VTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATS-DAICGDCLPGFYRKTKLV 128

Db        485 ENILNCGQHQCAELCHGGQCQPCQ--IILN--QVCYCGSTSRDVLCGTDV------GKSD 534

Qy        129 GFQDMEC-------VPCGD--------PPP-------PYEPHC--ASKVNLVKIASTASS 164

Db        535 GFGDFSCLKTCGKDLKCGNHTCSQVCHPQPCQQCPRLPQLVRCCPCGQTPLSQLLELGSS 594

Qy        165 PRDTALAAV-----IC-SALATVLLALLILC---------------VIYCKRQFMEKK- 201

Db        595 SRKTCMDPVPSCGKVCGKPLPCGSLDFIHTCEKLCHEGDCGPVSRTSVISCRCSFRTKEL 654

Qy        202 PSWSLRSQDI--------------QYNGSELSCFDRPQ-------------LH---EYA 230

Db        655 PCTSLKSEDATFMCDKRCNKKRLCGRHKCNEICCVDKEHKCPLNCGRKLRCGLHRCEEPC 714

Qy        231 HRACCQ-CRRDSVQT----CGPVRLLPSMCC-------------------------EE 258

Db        715 HRGNCQTCWQASFDELTCHCGASVIYPPVPCGTRPPECTQTCARVHECDHPVYHSGHSEE 774

Qy        259 ACS-------------------------------PNPATLGCGVHSAASL---------- 277

Db        775 KCPPCTFLTQKWCMGKHEFRSNIPCHLVDISCGLPCSATLPCGMHKCQRLCHKGECLVDE 834

Qy        278 --------------------------------QAR-----NAGPAGEMVPTFFGSLTQSI 300

Db        835 PCKQPCTTPRADCGHPCMAPCHTSSPCPVTACKAKVELQCECGRRKEMVICSEASSTYQR 894

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db        895 IAAISMASKITDMQLGGS----VEISKLITKKEVHQARLECDEECSALERKKR--LAEAF 948

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAII 406

Db        949 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 992


RESULT 9
GQRTT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.3%;  Score 141.5;  DB 1;  Length 461;
  Best Local Similarity   21.6%;  Pred. No. 0.004;
  Matches   72;  Conservative   37;  Mismatches  113;  Indels  111;  Gaps   20;

Qy         34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCL 93

Db         44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCP-SPGQETVCEVCDKGTFTASQ--NHVRQCL 100

Qy         94 DCAVVNR--FQK--ANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPC----------- 138

Db        101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

Qy        139 ---------------GDPPPPYEPHCASKVNLVKI----ASTASSPRDTALAAVICSALA 179

Db        161 KQNTVCNCHAGFFLSGNECTPCS-HCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIF 219

Qy        180 TVLLALLILCV-IYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCR 238

Db        220 LGLCLLFFICISLLC------RYPQW-----------------RPRVYSII------C- 248

Qy        239 RDSVQTCGPVR-----------LLPSMCCEEACSPNPA---TLGCGV-----HSAASLQA 279

Db        249 RDS----APVKEVEGEGIVTKPLTPASI--PAFSPNPGFNPTLGFSTTPRFSHPVSSTPI 302

Qy        280 RNA-GPAG---------EMVPT------FFGSL 296

Db        303 SPVFGPSNWHNFVPPVREVVPTQGADPLLYGSL 335


RESULT 10
A26431
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.0%;  Score 135;  DB 1;  Length 425;
  Best Local Similarity   20.5%;  Pred. No. 0.011;
  Matches   84;  Conservative   53;  Mismatches  172;  Indels  100;  Gaps   20;

Qy         16 LLVLLGYLS--CKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCV 73
```

```
                ||::||  |   | || :|          || |  |  |  |  ::: ||        |
Db         18 LLLILGVSSGGAKETCSTG------LYTHSGEC--CKACNLGEGVAQPCG---ANQTVCE 66

Qy         74 TCRLHRFKED--WGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKTK----- 126
               |  :   |     : |||| :|  : :   | |    ||:|  |  |:|:  :
Db         67 PCLDNVTFSDVVSATEPCKPCTECLGL-QSMSAPCVEADDAVC-RCAYGYYQDEETGHCE 124

Qy        127 -----------LVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVIC 175
                        :   || :   | : |   |   : : | |          |  |   :|
Db        125 ACSVCEVGSGLVFSCQDKQNTVCEECP---EGTYSDEANHV----------DPCLPCTVC 171

Qy        176 SALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACC 235
                  |     | :   :  |   | ||   : : |       |::
Db        172 EDTERQLRE----CTPWADAECEEIPGRWIPRSTPPEGSDSTAPSTQEPEVPP------- 220

Qy        236 QCRRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGS 295
                :|         :||   :   :    :|      :|      |    ::| :
Db        221 --EQD---------LVPSTVADMVTT----VMG------SSQPVVTRGTTDNLIPVYCSI 259

Qy        296 LTQSICGEFS----DAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNS 351
              |   : |  :       |   :    | |    :  |   || :||     :|  |:|| |
Db        260 LAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQTPPPEGEKLHS-----DSGISVDSQS 314

Qy        352 SQDLVGGAVPVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQ 400
                |        |:|::  ||:    : :  |  |      || | ::::
Db        315 LHD-------QQTHTQ--TASGQALKGDGNLYSSL----PLTKREEVEK 350


RESULT 11
S53457
dominant autoantigen gp 330 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C;Accession: S53457
R;Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A;Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of acti
A;Reference number: S53457; MUID:95151000; PMID:7848267
A;Accession: S53457
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1650 <JOK>
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;72-106/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;111-147/Domain: EGF homology <EG1>
F;153-188/Domain: EGF homology <EG2>
F;196-235/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;236-278/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F;279-329/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F;330-373/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F;374-414/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F;415-457/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;466-505/Domain: EGF homology <EG3>
F;509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;550-586/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F;595-631/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;636-672/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;679-715/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;720-755/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;760-794/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;799-833/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;843-879/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;884-921/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F;929-963/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;971-1006/Domain: EGF homology <EG4>
F;1012-1048/Domain: EGF homology <EG5>
F;1055-1099/Domain: LDL receptor YWTD-containing repeat homology #status atypical <YW07>
F;1100-1154/Domain: LDL receptor YWTD-containing repeat homology #status atypical <YW08>
F;1155-1188/Domain: LDL receptor YWTD-containing repeat homology #status atypical <YW09>
F;1189-1232/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;1234-1273/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F;1274-1316/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F;1326-1359/Domain: EGF homology <EG6>

  Query Match              5.9%;  Score 133;  DB 2;  Length 1650;
  Best Local Similarity   23.1%;  Pred. No. 0.07;
  Matches   97;  Conservative   45;  Mismatches  144;  Indels  134;  Gaps   30;

Qy         29 CESGDCRQQEFRDRSGNCVPCN-QCGPGMELSKECGFGYGEDA--QCVT----------- 74
                | |  ||  :|:  :| |:| : :|    ::  :||  | ::   :| |
Db        631 CASRTCRPGQFKCNNGRCIPQSWKC----DVDNDCG-DYSDEPIDECTTAAYNCDNHTEF 685

Qy         75 -CRL-HRFKEDW----GFQKCKPCLD--------CAVVNRFQKAN---------CSATSD 111
               |:  :|    |    ||  |:  |        |     |: ||         | | |
Db        686 SCKTNYRCIPQWAVCNGFDDCRENSDEQGCESVPCHPSGDFRCANHHCIPLRWKCDGTDD 745

Qy        112 AICGD------CLPGFYRKTKLVGFQ--DMECVP----------CGD-----------P 141
                |||       |:|   |:     |:  | :|:|          |||
Db        746 --CGDNSDEENCVP---RECSESEFRCADQQCIPSRWVCDQENDCGDNSDERDCEMKTCH 800

Qy        142 PPPYE---PHCASKVNLVKIASTASSPRDTALAAVICSAL------ATVLLALLILCVIY 192
                |  ::    ||  |       : |  |  | |  ||          |   | :  |  :
Db        801 PEHFQCTSGHCVPK-------ALACDGRADCLDASDESACPTRFPNGTYCPAAMFECKNH 853

Qy        193 -CKRQFMEKKPSWSLRSQDIQYNGSELS---CF----DRPQLHE-------YAHRACCQC 237
                | : |       |    ::   :||:     ||    : ||           | |: |
Db        854 VCIQSF------WICDGENDCVDGSDEEIHLCFNIPCESPQRFRCDNSRCVYGHQLC--- 904

Qy        238 RRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLT 297
                : |  ||      |  || |  |    |  :    :  |    |  :  :
Db        905 --NGVDDCGD----GSDEKEEHCR-KPTHKPC---TDTEYKCSN----GNCISQHYVCDN 950

Qy        298 QSICGEFSD--AWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDL 355
                : ||: ||      |  |    :||  :    :|  | | |  : |||  | ||  ||:
Db        951 VNDCGDLSDETGCNLGDNRTCAENICEQNCTQLSSGGFICSCRPGFKPSTS-DKNSCQDI 1009


RESULT 12
T42737
gp330 protein precursor - rat
N;Alternate names: megalin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of tl
A;Reference number: A58173; MUID:95024033; PMID:7937880
A;Accession: T42737
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4660 <SAI>
A;Cross-references: EMBL:L34049; NID:g561852; PID:g561853; PIDN:AAA51369.1
A;Experimental source: strain Sprague-Dawley; kidney
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <MAT>

  Query Match              5.9%;  Score 133;  DB 2;  Length 4660;
  Best Local Similarity   23.1%;  Pred. No. 0.21;
  Matches   97;  Conservative   45;  Mismatches  144;  Indels  134;  Gaps   30;

Qy         29 CESGDCRQQEFRDRSGNCVPCN-QCGPGMELSKECGFGYGEDA--QCVT----------- 74
                | |  ||  :|:  :| |:| : :|    ::  :||  | ::   :| |
Db       3632 CASRTCRPGQFKCNNGRCIPQSWKC----DVDNDCG-DYSDEPIDECTTAAYNCDNHTEF 3686

Qy         75 -CRL-HRFKEDW----GFQKCKPCLD--------CAVVNRFQKAN---------CSATSD 111
               |:  :|    |    ||  |:  |        |     |: ||         | | |
Db       3687 SCKTNYRCIPQWAVCNGFDDCRDNSDEQGCESVPCHPSGDFRCANHHCIPLRWKCDGTDD 3746

Qy        112 AICGD------CLPGFYRKTKLVGFQ--DMECVP----------CGD-----------P 141
                |||       |:|   |:     |:  | :|:|          |||
Db       3747 --CGDNSDEENCVP---RECSESEFRCADQQCIPSRWVCDQENDCGDNSDERDCEMKTCH 3801

Qy        142 PPPYE---PHCASKVNLVKIASTASSPRDTALAAVICSAL------ATVLLALLILCVIY 192
```

```
                |  ::    ||  |       : |   |   | |   ||         |   | :  |  :
Db       3802 PEHFQCTSGHCVPK-------ALACDGRADCLDASDESACPTRFPNGTYCPAAMFECKNH 3854

Qy        193 -CKRQFMEKKPSWSLRSQDIQYNGSELS---CF----DRPQLHE-------YAHRACCQC 237
                | : |      |    ::   :||:     ||    : ||           | |: |
Db       3855 VCIQSF------WICDGENDCVDGSDEEIHLCFNIPCESPQRFRCDNSRCVYGHQLC--- 3905

Qy        238 RRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLT 297
              : |  ||       |   ||| |   |     |   :   : |     |  :   :
Db       3906 --NGVDDCGD----GSDEKEEHCR-KPTHKPC---TDTEYKCSN----GNCISQHYVCDN 3951

Qy        298 QSICGEFSD--AWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDL 355
              : ||: ||     |  |    :||   :     :|  | |  |  : ||| | || ||:
Db       3952 VNDCGDLSDETGCNLGDNRTCAENICEQNCTQLSSGGFICSCRPGFKPSTS-DKNSCQDI 4010
```

RESULT 13
VWHU
von Willebrand factor precursor - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A34480; S02377; A37139; S23676; A25298; A25469; A25366; S23618; S23645; A94
R;Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora
J. Biol. Chem. 264, 19514-19527, 1989
A;Title: Structure of the gene for human von Willebrand factor.
A;Reference number: A34480; MUID:90062044; PMID:2584182
A;Accession: A34480
A;Molecule type: DNA
A;Residues: 1-2813 <MAN>
A;Cross-references: EMBL:M25864
R;Bonthron, D.; Orkin, S.H.
Eur. J. Biochem. 171, 51-57, 1988
A;Title: The human von Willebrand factor gene. Structure of the 5' region.
A;Reference number: S02377; MUID:88111704; PMID:2828057
A;Accession: S02377
A;Molecule type: DNA
A;Residues: 1-177 <BO2>
A;Cross-references: EMBL:X06828
R;Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora
Biochemistry 30, 253-269, 1991
A;Title: Human von Willebrand factor gene and pseudogene: structural analysis and differ
A;Reference number: A37139; MUID:91105089; PMID:1988024
A;Accession: A37139
A;Molecule type: DNA
A;Residues: 990-1947 <MAD>
A;Cross-references: GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:g553810
A;Note: the authors translated the codon CGC for residue 156 as Gln
R;Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A;Title: Molecular cloning of the human gene for von Willebrand factor and identificatic
A;Reference number: S23676; MUID:87260814; PMID:3496594
A;Accession: S23676
A;Molecule type: DNA
A;Residues: 2731-2813 <COL>
A;Cross-references: EMBL:M16945
R;Bonthron, D.; Orr, E.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A;Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A;Reference number: A25298; MUID:87016349; PMID:3489923
A;Accession: A25298
A;Molecule type: mRNA
A;Residues: 1-470,'V',472-2813 <BON>
A;Cross-references: EMBL:X04385
R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 1839-1847, 1986
A;Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei
A;Reference number: A91044; MUID:87004550; PMID:3019665
A;Accession: A25469
A;Molecule type: mRNA
A;Residues: 1-470,'V',472-483,'R',485-1022,'K',1024-1025,'E',1027-1400 <VER>
A;Cross-references: EMBL:X04146
A;Note: this sequence has been revised in reference A91056
R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 3074, 1986
A;Reference number: A91056
A;Accession: A25366
A;Molecule type: mRNA
A;Residues: 1021-1030 <VE2>
A;Note: this is a revision to the sequence from reference A91044
R;Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A;Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated
A;Reference number: S23618; MUID:87213253; PMID:3495266
A;Accession: S23618
A;Molecule type: mRNA
A;Residues: 1-120 <SH2>
A;Cross-references: EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PID:g340316
A;Accession: S23645
A;Molecule type: protein
A;Residues: 23-56 <SH3>
R;Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
A;Title: Cloning and characterization of two cDNAs coding for human von Willebrand facto
A;Reference number: A94060; MUID:86016708; PMID:2864688
A;Accession: A94060
A;Molecule type: mRNA
A;Residues: 'WA',739,'C',744-769,'H',771-788,'A',790-803,'S',805-873;1289-1471,'D',1473-
A;Note: the authors translated the codon TCG for residue 2168 as Cys
R;Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
Biochemistry 25, 3164-3171, 1986
A;Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc
A;Reference number: A90504; MUID:86269894; PMID:3488076
A;Accession: A90504
A;Molecule type: mRNA
A;Residues: 781-788,'A',790-1424 <SHE>
A;Note: 852-Gln, 857-Asp, and 1381-Thr were also found
R;Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; O
Science 228, 1401-1406, 1985
A;Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones
A;Reference number: A44178; MUID:85244588; PMID:3874428
A;Accession: A44178
A;Molecule type: mRNA
A;Residues: 2621-2813 <GIN>
A;Cross-references: EMBL:K03028; NID:g340308; PIDN:AAA61293.1; PID:g340309
R;Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; va
Nucleic Acids Res. 13, 4699-4717, 1985
A;Title: Construction of cDNA coding for human von Willebrand factor using antibody prob
A;Reference number: S07363; MUID:85269603; PMID:3875078
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2731-2813 <VE3>
A;Cross-references: EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PID:g37940
R;Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livin
Cell 41, 49-56, 1985
A;Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a
A;Reference number: S23678; MUID:85201687; PMID:3873280
A;Accession: S23678
A;Molecule type: mRNA
A;Residues: 2731-2813 <LYN>
A;Cross-references: EMBL:K03028
R;Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;
Biochemistry 25, 3171-3184, 1986
A;Title: Amino acid sequences of human von Willebrand factor.
A;Reference number: A90505; MUID:86269895; PMID:3524673
A;Accession: A90505
A;Molecule type: protein
A;Residues: 764-788,'A',790-1471,'D',1473-2813 <TIT>
A;Note: 789-Thr was also found
R;Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
A;Title: Human von Willebrand factor: a multivalent protein composed of identical subuni
A;Reference number: A23464; MUID:86269892; PMID:3015199
A;Accession: A23464
A;Molecule type: protein
A;Residues: 764-773;2803-2813 <CHO>
R;Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.
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Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A;Title: Identification of a cleavage site directing the immunochemical detection of mol
A;Reference number: A36013; MUID:90349604; PMID:2385594
A;Accession: A36013
A;Molecule type: protein
A;Residues: 1606-1617 <DEN>
R;Fay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
Science 232, 995-998, 1986
A;Title: Propolypeptide of von Willebrand factor circulates in blood and is identical to
A;Reference number: A60913; MUID:86208144; PMID:3486471
A;Accession: A60913
A;Molecule type: protein
A;Residues: 576-590 <FAY>
C;Genetics:
A;Gene: GDB:VWF
A;Cross-references: GDB:119125; OMIM:193400
A;Map position: 12p13.3-12p13.2
A;Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1; 51
5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2200/1; 2266/3; 230
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C;Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-763/Product: von Willebrand antigen II #status predicted <MA1>
F;34-386/Domain: type D repeat 1 <DD1>
F;387-745/Domain: type D repeat 2 <DD2>
F;698-700/Region: cell attachment (R-G-D) motif
F;764-2813/Product: von Willebrand factor #status predicted <MA2>
F;784-865/Domain: D' <DDD>
F;788-833,2216-2261/Region: duplication
F;826-853,2400-2515,2544-2662/Region: duplication
F;842-1130,1934-2203/Region: duplication
F;866-1241/Domain: type D repeat 3 <DD3>
F;1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>
F;1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
F;1947-2295/Domain: type D repeat 4 <DD4>
F;2296-2330/Domain: type B repeat 1 <VB1>
F;2340-2365/Domain: type B repeat 2 <VB2>
F;2375-2399/Domain: type B repeat 3 <VB3>
F;2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>
F;2507-2509/Region: cell attachment (R-G-D) motif
F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F;857,1231,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (Asn)
F;1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F;1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent) #s
F;1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             5.9%;  Score 132.5;  DB 1;  Length 2813;
  Best Local Similarity   21.4%;  Pred. No. 0.14;
  Matches   78;  Conservative   38;  Mismatches  107;  Indels  141;  Gaps   19;

Qy         44 GNCVP---CNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNR 100
              |:|||   | ||               |||        |:| | |     :|| |  ::
Db       2246 GSCVPEEACTQC------------IGEDGV-----QHQFLEAW-VPDHQPCQICTCLSG 2286

Qy        101 FQKANCSA----TSDA-ICGDCLPGFYRKTKLVGFQDMEC----VPCGDPPPPYEPHCAS 151
               :| ||:     |: |  || |     |:      : ||    | |  ||    |||
Db       2287 -RKVNCTTQPCPTAKAPTCGLCEVARLRQNADQCCPEYECVCDPVSCDLPP---VPHCER 2342

Qy        152 KVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDI 211
                 :  | ::| :                          |:  |
Db       2343 -----GLQPTLTNPGE------------------------CRPNF------------- 2358

Qy        212 QYNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSM----CCEE---ACSPNP 264
                 :|  | :          :|:| |  :| | | ||::    ||:|   ||:
Db       2359 -------TCACRKE----------ECKRVSPPSCPPHR-LPTLRKTQCCDEYECACNCVN 2400

Qy        265 ATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSICGEFSDAWPL-------------- 310
               :|: | :   ||    : |       |    |   :|   |  :|:
Db       2401 STVSCPLGYLASTATNDCG------CTTTTCLPDKVCVHRSTIYPVGQFWEEGCDVCTCT 2454

Qy        311 -MQNPMGGDNISFCDSYP---------------ELTGEDIHSLNPELESSTSLDSNSSQ 353
                |:: : |  :: |   |               |  |  : |    :  |   || ||
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Db       2455 DMEDAVMGLRVAQCSQKPCEDSCRSGFTYVLHEGECCGRCLPSACEVVTGSPRGDSQSSW 2514

Qy         354 DLVG 357
                ||
Db       2515 KSVG 2518


RESULT 14
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             5.9%;  Score 132;  DB 2;  Length 277;
  Best Local Similarity   24.6%;  Pred. No. 0.012;
  Matches   52;  Conservative   27;  Mismatches   78;  Indels   54;  Gaps   11;

Qy         34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWG-------F 86
              ||::::   |  |  |: | || :|  :|      : :|: |     | : |
Db         26 CREKQYLINS-QC--CSLCQPGQKLVSDC--TEFTETECLPCGESEFLDTWNRETHCHQH 80

Qy         87 QKCKPCLDCAVVNRFQKANCSATSDAIC-------------------GDCLPGFYRKTKL 127
              : | | |      | |:   | | | ||                    | |||  |
Db         81 KYCDPNLGL----RVQQKGTSET-DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA 135

Qy        128 VGFQDMECVPC-----GDPPPPYE-----PHCASKVNLVKIAST-----ASSPRDTALAA 172
                |  |  | ||      :    :|       | :|  :|: | |        |:|   |
Db        136 TGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQDRLRAL 195

Qy        173 VICSALATVLLALLILCVIYCKRQFMEKKPS 203
              |:   :  :| |:|:: |   |   : |||:
Db        196 VVIPIIFGILFAILLVLVFIKK---VAKKPT 223


RESULT 15
MMMSB1
laminin beta-1 chain precursor - mouse
N;Alternate names: laminin chain B1
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C;Accession: A26413; S02679; S05326; S14877; A02871; S02036; S13543
R;Sasaki, M.; Kato, S.; Kohno, K.; Martin, G.R.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. 84, 935-939, 1987
```

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A;Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protei
A;Reference number: A26413; MUID:87147212; PMID:3493487
A;Accession: A26413
A;Molecule type: mRNA
A;Residues: 1-1786 <SAS>
A;Cross-references: EMBL:M15525; NID:g198700
A;Note: translation in GenBank has additional 48 residues at the amino end
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domair
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02679
A;Molecule type: protein
A;Residues: 28-42;932-946 <FUJ>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S05326
A;Molecule type: protein
A;Residues: 457-466;854-868;932-946 <HAR>
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S14877
A;Molecule type: protein
A;Residues: 590-620 <MAN>
R;Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.
EMBO J. 3, 2355-2362, 1984
A;Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a
A;Reference number: A02870; MUID:85051302; PMID:6209134
A;Accession: A02871
A;Molecule type: mRNA
A;Residues: 1292-1530,'MEMP',1535-1691,'C',1693-1748,'N',1750-1786 <BAR>
A;Cross-references: EMBL:X05212; NID:g52861; PIDN:CAA28839.1; PID:g809042
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S02036
A;Molecule type: protein
A;Residues: 1561-1587 <DEU>
R;Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.
EMBO J. 4, 309-316, 1985
A;Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.
A;Reference number: S13543; MUID:85257455; PMID:3848400
A;Accession: S13543
A;Molecule type: protein
A;Residues: 1700-1748,'N',1750-1759 <PAU>
C;Genetics:
A;Gene: Lamb-1
A;Map position: 12
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>
F;22-270/Domain: VI <DOM6>
F;271-540/Domain: V <DOM5>
F;271-332/Domain: laminin-type EGF-like homology <LE01>
F;335-395/Domain: laminin-type EGF-like homology <LE02>
F;398-455/Domain: laminin-type EGF-like homology <LE03>
F;458-507/Domain: laminin-type EGF-like homology <LE04>
F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;541-772/Domain: IV <DOM4>
F;773-1182/Domain: III <DOM3>
F;773-818/Domain: laminin-type EGF-like homology <LE06>
F;821-864/Domain: laminin-type EGF-like homology <LE07>
F;867-914/Domain: laminin-type EGF-like homology <LE08>
F;917-973/Domain: laminin-type EGF-like homology <LE09>
F;976-1025/Domain: laminin-type EGF-like homology <LE10>
F;1028-1081/Domain: laminin-type EGF-like homology <LE11>
F;1084-1129/Domain: laminin-type EGF-like homology <LE12>
F;1132-1176/Domain: laminin-type EGF-like homology <LE13>
F;1183-1397/Domain: II <DOM2>
F;1183-1397/Region: heptad repeats
F;1398-1430/Domain: alpha <ALP>
F;1431-1786/Region: heptad repeats
F;1431-1786/Domain: I <DOM1>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;30-35/Disulfide bonds: #status predicted
F;120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydrat
F;1179,1182,1785/Disulfide bonds: interchain #status predicted

  Query Match             5.9%;  Score 132;  DB 1;  Length 1786;
  Best Local Similarity   20.6%;  Pred. No. 0.09;
  Matches   83;  Conservative   32;  Mismatches  125;  Indels  162;  Gaps   24;

Qy         21 GYLSCKVTCESGDCRQQEFRDRSGNCVP------CNQCGPGMELSKECGFGYGED----- 69
                | ||        | |:        | |       ||:| ||        ||:| :
Db        779 GSLSSVCDPNGGQCQ-----------CRPNVVGRTCNRCAPGT-------FGFGPNGCKPC 821

Qy         70 -----------AQCVTCRLHRFK-----------EDWGFQKCKPC------LDCAVVNR 100
                         :| : | |:                |||  |:||      |||  |
Db        822 DCHLQGSASAFCDAITGQCHCFQGIYARQCDRCLPGYWGFPSCQPCQCNGHALDCDTVT- 880

Qy        101 FQKANCSATSDAI----CGDCLPGFYRKTKLVGFQDMECVPCGDPPPP-----YEPHCAS 151
                    | :  |       |  || |:|     ::|  |   | ||  |   |      :    |
Db        881 ---GECLSCQDYTTGHNCERCLAGYY-GDPIIGSGD-HCRPCPCPDGPDSGRQFARSCYQ 935

Qy        152 KVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDI 211
                  :::|         |                 |      |         :     |
Db        936 DPVTLQLACVC----DPGYIGSRCDD--------------CASGFFGNPSDFGGSCQPC 976

Qy        212 QYN---------------GSELSCF-----DRPQLHEYAH---------RAC-------- 234
              | :               |  |  |       |  || :| :             | |
Db        977 QCHHNIDTTDPEACDKDTGRCLKCLYHTEGDHCQLCQYGYYGDALRQDCRKCVCNYLGTV 1036

Qy        235 --------CQCRRDSVQ-TCGPVRLLPSMCCEEACSPNPATL----GCGVHSAASLQARN 281
                      | | : : | :|  |  ::   |   : |:||   |     |||  :  :  | :
Db       1037 KEHCNGSDCHCDKATGQCSCLP-NVIGQNC--DRCAPNTWQLASGTGCGPCNCNA--AHS 1091

Qy        282 AGPAGEMVPTFFGSLTQSICGEFSDAWPLMQNPMGGDNISFC 323
                ||:               | ||:       |      ||    | |
Db       1092 FGPS---------------CNEFTGQCQCMPG-FGGRTCSEC 1117

Search completed: January 29, 2004, 21:40:33
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:33:06 ; Search time 18 Seconds
(without alignments)
1089.452 Million cell updates/sec

Title: US-09-780-532A-2
Perfect score: 2256
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....LDQESGAIIHPATQTSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2246	99.6	423	1	TR19_HUMAN	Q9ns68 homo sapien
2	1565.5	69.4	416	1	TR19_MOUSE	Q9jll3 mus musculu
3	480.5	21.3	297	1	XEDA_HUMAN	Q9hav5 homo sapien
4	198	8.8	448	1	EDAR_MOUSE	Q9r187 mus musculu
5	191	8.5	448	1	EDAR_HUMAN	Q9une0 homo sapien
6	185	8.2	514	1	EDAR_ORYLA	Q90vy2 oryzias lat
7	157	7.0	454	1	TR1A_MOUSE	P25118 mus musculu
8	148	6.6	416	1	TR16_CHICK	P18519 gallus gall
9	146.5	6.5	435	1	TNR3_HUMAN	P36941 homo sapien
10	145	6.4	271	1	TNR4_RAT	P15725 rattus norv
11	144	6.4	272	1	TNR4_MOUSE	P47741 mus musculu
12	142.5	6.3	1801	1	LMB2_RAT	P15800 rattus norv
13	142	6.3	1104	1	NFX1_HUMAN	Q12986 homo sapien
14	141.5	6.3	461	1	TR1A_RAT	P22934 rattus norv
15	141	6.2	430	1	TRLT_MACFA	Q9n092 macaca fasc
16	138	6.1	417	1	TR16_MOUSE	Q9z0w1 mus musculu
17	136.5	6.1	430	1	TRLT_HUMAN	Q969z4 homo sapien
18	135	6.0	425	1	TR16_RAT	P07174 rattus norv
19	134.5	6.0	415	1	TNR3_MOUSE	P50284 mus musculu
20	133	5.9	625	1	TR11_MOUSE	O35305 mus musculu
21	133	5.9	4660	1	LRP2_RAT	P98158 rattus norv
22	132.5	5.9	1798	1	LMB2_HUMAN	P55268 homo sapien
23	132.5	5.9	2813	1	VWF_HUMAN	P04275 homo sapien
24	132	5.9	176	1	TR23_MOUSE	Q9er63 mus musculu
25	132	5.9	277	1	TNR5_HUMAN	P25942 homo sapien
26	132	5.9	1786	1	LMB1_MOUSE	P02469 mus musculu
27	131.5	5.8	1799	1	LMB2_MOUSE	Q61292 mus musculu
28	130.5	5.8	1170	1	TSP1_MOUSE	P35441 mus musculu
29	129	5.7	326	1	VT2_MYXVL	P29825 myxoma viru
30	126.5	5.6	471	1	TR1A_BOVIN	O19131 bos taurus
31	126.5	5.6	1170	1	TSP1_HUMAN	P07996 homo sapien
32	125.5	5.6	1696	1	PCK5_BRACL	Q9nj15 branchiosto
33	124.5	5.5	1587	1	LMG3_HUMAN	Q9y6n6 homo sapien
34	124	5.5	1170	1	TSP1_BOVIN	Q28178 bos taurus
35	123.5	5.5	830	1	SREC_HUMAN	Q14162 homo sapien
36	123.5	5.5	965	1	YNC3_YEAST	P53971 saccharomyc
37	123.5	5.5	1173	1	TSP1_XENLA	P35448 xenopus lae
38	123	5.5	256	1	TNR9_MOUSE	P20334 mus musculu
39	122.5	5.4	1877	1	PCK5_MOUSE	Q04592 mus musculu
40	122	5.4	349	1	CRMB_VARV	P34015 variola vir
41	122	5.4	1679	1	FUR2_DROME	P30432 drosophila
42	121.5	5.4	863	1	LDVR_CHICK	P98165 gallus gall
43	121.5	5.4	3695	1	LMA5_HUMAN	O15230 homo sapien
44	121	5.4	1786	1	LMB1_HUMAN	P07942 homo sapien
45	121	5.4	1964	1	NTC4_MOUSE	P31695 mus musculu

ALIGNMENTS

RESULT 1
TR19_HUMAN
ID TR19_HUMAN STANDARD; PRT; 423 AA.
AC Q9NS68; Q9BXZ9; Q9BY00; Q9NZV2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19 precursor
DE (Toxicity and JNK inducer) (TRADE).
GN TNFRSF19 OR TROY OR TAJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2;
RP TRAF3 AND TRAF5.
RC TISSUE=Fetal spleen;
RX MEDLINE=20270246; PubMed=10809768;
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a novel member of the tumor necrosis factor receptor family,
RT activates the c-Jun N-terminal kinase pathway and mediates
RT caspase-independent cell death.";
RL J. Biol. Chem. 275:15336-15342(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Glial tumor;
RX MEDLINE=20347167; PubMed=10764796;
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Chaudhary D., Long A.J.;
RT "TRADE, a novel TNF receptor family member associated with death
RT signaling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Can mediate activation of JNK and NF-kappa-B. May
CC promote caspase-independent cell death.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=TAJ-alpha, TRADEalpha;
CC IsoId=Q9NS68-1; Sequence=Displayed;
CC Name=2; Synonyms=TRADEbeta;
CC IsoId=Q9NS68-2; Sequence=VSP_006512;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in prostate. Detected at
CC lower levels in thymus, spleen, testis, uterus, small intestine,
CC colon and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC ---

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CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; AF167555; AAF71828.1; -.
DR   EMBL; AB040434; BAB03269.1; -.
DR   EMBL; AF246998; AAK28395.1; -.
DR   EMBL; AF246999; AAK28396.1; -.
DR   Genew; HGNC:11915; TNFRSF19.
DR   MIM; 606122; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; NAS.
DR   GO; GO:0006917; P:induction of apoptosis; NAS.
DR   GO; GO:0007254; P:JNK cascade; NAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Alternative splicing.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    423       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 19.
FT   DOMAIN       30    170       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    171    191       POTENTIAL.
FT   DOMAIN      192    423       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       33     72       TNFR-CYS 1.
FT   REPEAT       74    114       TNFR-CYS 2.
FT   REPEAT      116    149       TNFR-CYS 3.
FT   DISULFID     34     46       BY SIMILARITY.
FT   DISULFID     49     62       BY SIMILARITY.
FT   DISULFID     52     72       BY SIMILARITY.
FT   DISULFID     75     89       BY SIMILARITY.
FT   DISULFID     92    106       BY SIMILARITY.
FT   DISULFID     95    114       BY SIMILARITY.
FT   DISULFID    117    135       BY SIMILARITY.
FT   DISULFID    138    149       BY SIMILARITY.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    416    423       VRQRLGSL -> EA (in isoform 2).
FT                                /FTId=VSP_006512.
FT   CONFLICT     31     31       S -> T (IN REF. 3; AAK28396).
FT   CONFLICT     74     74       T -> A (IN REF. 1).
FT   CONFLICT    215    216       GS -> ET (IN REF. 1).
FT   CONFLICT    221    221       F -> L (IN REF. 3; AAK28396).
FT   CONFLICT    330    330       T -> A (IN REF. 3; AAK28396).
FT   CONFLICT    405    405       V -> I (IN REF. 3).
SQ   SEQUENCE   423 AA;  46015 MW;  B5891CEA9ED45361 CRC64;

  Query Match             99.6%;  Score 2246;  DB 1;  Length 423;
  Best Local Similarity   99.8%;  Pred. No. 3e-163;
  Matches  414;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQ 415
              |||||||||||||||||||||||||||||||||||||:||||||||||
Db        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQ 415


RESULT 2
TR19_MOUSE
ID   TR19_MOUSE     STANDARD;      PRT;   416 AA.
AC   Q9JLL3; Q9JHF1; Q9JJH6; Q9JLL2; Q9QXW7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 19 precursor
DE   (Toxicity and JNK inducer) (TRADE).
GN   TNFRSF19 OR TROY OR TAJ.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 4).
RX   MEDLINE=20054362; PubMed=10585776;
RA   Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
RT   "Characterization of TNFRSF19, a novel member of tumor necrosis factor
RT   receptor superfamily.";
RL   Genomics 62:103-107(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   TISSUE=Embryo, and Spleen;
RX   MEDLINE=20270246; PubMed=10809768;
RA   Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT   "TAJ, a novel member of the tumor necrosis factor receptor family,
RT   activates the c-Jun N-terminal kinase pathway and mediates
RT   caspase-independent cell death.";
RL   J. Biol. Chem. 275:15336-15342(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC   TISSUE=Brain;
RX   MEDLINE=20347167; PubMed=10764796;
RA   Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Senba E., Kitamura T.;
RT   "TROY, a newly identified member of the tumor necrosis factor receptor
RT   superfamily, exhibits a homology with Edar and is expressed in
RT   embryonic skin and hair follicles.";
RL   J. Biol. Chem. 275:20742-20747(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6;
RA   Chaudhary D., Long A.J.;
RT   "TRADE, a novel TNF receptor family member associated with death
RT   signaling.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Can mediate activation of c-Jun and NF-kappa-B. May
CC       promote caspase-independent cell death (By similarity). Isoform 2
CC       and isoform 3 may act as decoy receptors.
CC   -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 3 and
CC       4); Secreted (isoform 2) (Probable).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=TAJ-alphaL;
CC         IsoId=Q9JLL3-1; Sequence=Displayed;
CC       Name=2; Synonyms=TAJ-beta1;
CC         IsoId=Q9JLL3-2; Sequence=VSP_006513, VSP_006514;
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CC       Name=3; Synonyms=TAJ-alphaS, dTROY;
CC         IsoId=Q9JLL3-3; Sequence=VSP_006515, VSP_006516;
CC       Name=4;
CC         IsoId=Q9JLL3-4; Sequence=VSP_006517, VSP_006518;
CC   -!- TISSUE SPECIFICITY: Highly expressed in adult brain, and in
CC       embryos from day 11-17, but not earlier. Detected in embryonic
CC       brain and epithelium, and at lower levels in adult heart, lung and
CC       liver. In neonatal mice, mainly in hair follicles and neuron-like
CC       cells in the cerebellum, but not in the skin epidermis. Isoform 3
CC       was found in embryonic day 17.5 skin but not in brain and liver.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF173166; AAF19795.1; -.
DR   EMBL; AF167552; AAF71825.1; -.
DR   EMBL; AF167554; AAF71827.1; -.
DR   EMBL; AF167553; AAF71826.1; -.
DR   EMBL; AB040432; BAB03267.1; -.
DR   EMBL; AB040433; BAB03268.1; -.
DR   EMBL; AF247000; AAK28397.1; -.
DR   MGD; MGI:1352474; Tnfrsf19.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Alternative splicing.
FT   SIGNAL       1     29       POTENTIAL.
FT   CHAIN       30    416       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 19.
FT   DOMAIN      30    170       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   171    191       POTENTIAL.
FT   DOMAIN     192    416       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      33     72       TNFR-CYS 1.
FT   REPEAT      74    114       TNFR-CYS 2.
FT   REPEAT     116    149       TNFR-CYS 3 (PARTIAL).
FT   DISULFID    34     46       BY SIMILARITY.
FT   DISULFID    49     62       BY SIMILARITY.
FT   DISULFID    52     72       BY SIMILARITY.
FT   DISULFID    75     89       BY SIMILARITY.
FT   DISULFID    92    106       BY SIMILARITY.
FT   DISULFID    95    114       BY SIMILARITY.
FT   DISULFID   117    135       BY SIMILARITY.
FT   DISULFID   138    149       BY SIMILARITY.
FT   CARBOHYD   105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC   150    150       T -> E (in isoform 2).
FT                               /FTId=VSP_006513.
FT   VARSPLIC   151    416       Missing (in isoform 2).
FT                               /FTId=VSP_006514.
FT   VARSPLIC   204    214       WSLRSQDIQYN -> CKLPSLCLTVK (in isoform
FT                               3).
FT                               /FTId=VSP_006515.
FT   VARSPLIC   215    416       Missing (in isoform 3).
FT                               /FTId=VSP_006516.
FT   VARSPLIC   340    348       NESTASLDS -> MLCFRFRDL (in isoform 4).
FT                               /FTId=VSP_006517.
FT   VARSPLIC   349    416       Missing (in isoform 4).
FT                               /FTId=VSP_006518.
FT   CONFLICT    31     31       T -> A (IN REF. 1).
FT   CONFLICT   208    208       S -> P (IN REF. 1).
FT   CONFLICT   287    287       N -> D (IN REF. 3).
FT   CONFLICT   343    343       T -> A (IN REF. 3).
SQ   SEQUENCE   416 AA;  45294 MW;  19CA2F75DD7B9D49 CRC64;

  Query Match             69.4%;  Score 1565.5;  DB 1;  Length 416;
  Best Local Similarity   70.4%;  Pred. No. 1.3e-111;
  Matches  295;  Conservative   35;  Mismatches   84;  Indels    5;  Gaps    3;

Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              |||||         |  :: | :|:|||:||:||||||||:|||||| | ||||||||||
Db          1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              |||||||||||| || |||||||||||||| |||:|||||:|||| ||||:|||||||
Db         61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              |||||||||||||||||||||||||||||| ||||||||:|| ||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180

Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              |||||||||||||||||||||||||||||||||||||||||:|:|    |||||||  ||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDQPRLRHCAHRACCQYHRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              |    ||| |:||:||||| |   | ||||: |  :|| ||    |  :| ||||:::||
Db        241 SAPMYGPVHLIPSLCCEEARSSARAVLGCGLRSPTTLQERNPASVGNTMPAFFGSVSRSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              | |||||||||||:|||: | |||||||||| :||||| ||: ||||:  ||| | |
Db        301 CAEFSDAWPLMQNPLGGDS-SLCDSYPELTGEDTNSLNPENESTASLDSSGGQDLAGTA- 358

Qy        361 PVQSHSENFTAATDLSRYNN--TLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
                  | | : :||  |: :  |: |    |||    ||   |    :: |  |: |:|
Db        359 -ALESSGNVSESTDSPRHGDTGTVWEQTLAQDAQRTPSQGGWEDRENLNLAMPTAFQDA 416


RESULT 3
XEDA_HUMAN
ID   XEDA_HUMAN     STANDARD;      PRT;   297 AA.
AC   Q9HAV5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member XEDAR (X-linked
DE   ectodysplasin-A2 receptor) (EDA-A2 receptor).
GN   XEDAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256.
RC   TISSUE=Fetal kidney;
RX   MEDLINE=20495245; PubMed=11039935;
RA   Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA   de Vos A.M., Gao W.-Q., Dixit V.M.;
RT   "Two-amino acid molecular switch in an epithelial morphogen that
RT   regulates binding to two distinct receptors.";
RL   Science 290:523-527(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform
CC       A1. Mediates the activation of NF-kappa-B. Activation seems to
CC       be mediated by binding to TRAF6.
CC   -!- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.
CC   -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF298812; AAG28761.1; -.
DR   EMBL; BC034919; AAH34919.1; -.
DR   MIM; 300276; -.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; NAS.
DR   GO; GO:0008544; P:epidermal differentiation; NAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Developmental protein; Differentiation; Transmembrane;
KW   Glycoprotein; Repeat.
FT   DOMAIN        1    138       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    139    159       SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN      160    297       CYTOPLASMIC (POTENTIAL).
FT   REPEAT        2     41       TNFR-CYS 1.
FT   REPEAT       43     83       TNFR-CYS 2.
FT   REPEAT       85    118       TNFR-CYS 3.
FT   DISULFID      3     15       BY SIMILARITY.
FT   DISULFID     18     31       BY SIMILARITY.
FT   DISULFID     21     41       BY SIMILARITY.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     61     75       BY SIMILARITY.
FT   DISULFID     64     83       BY SIMILARITY.
FT   DISULFID     86    104       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   CARBOHYD     74     74       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN     256    256       E->R: ABOLISHES TRAF6 ASSOCIATION.
SQ   SEQUENCE   297 AA;  32728 MW;  0E71127C6C48240C CRC64;

  Query Match             21.3%;  Score 480.5;  DB 1;  Length 297;
  Best Local Similarity   39.7%;  Pred. No. 1.8e-29;
  Matches   91;  Conservative   34;  Mismatches   97;  Indels    7;  Gaps    1;

Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |: |: | || | :|||| ||||:||:| | || |  |   |:|  ||  :|: |
Db          2 DCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQSC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| || ||:|||:|:|||||| |||||:: | || ||:||    |  |  || :
Db         62 ITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQ 212
              ::||:  :    |::  | |:: | |    || | |  :|||: |         |   :
Db        122 LSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEAD 181

Qy        213 YNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACS 261
                | | |  |   | :  :       |   |:       |: ||
Db        182 KTAKEESLFPVPPSKETSAESQVSENIFQTQPLNPI-------LEDDCS 223
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RESULT 4
EDAR_MOUSE
ID   EDAR_MOUSE     STANDARD;      PRT;   448 AA.
AC   Q9R187; Q9DC43;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member EDAR precursor
DE   (Anhidrotic ectodysplasin receptor 1) (Ectodysplasin-A receptor)
DE   (Ectodermal dysplasia receptor) (Downless).
GN   EDAR OR DL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT LYS-379.
RC   TISSUE=Embryonic foot, Embryonic skin, and Embryonic tail;
RX   MEDLINE=99364417; PubMed=10431242;
RA   Headon D.J., Overbeek P.A.;
RT   "Involvement of a novel Tnf receptor homologue in hair follicle
RT   induction.";
RL   Nat. Genet. 22:370-374(1999).
RN   [2]
RP   SEQUENCE OF 205-448 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   INDUCTION BY ACTIVIN A.
RX   MEDLINE=21077039; PubMed=11203701;
RA   Laurikkala J., Mikkola M.L., Mustonen T., Aaberg T., Koppinen P.,
RA   Pispa J., Nieminen P., Galceran J., Grosschedl R., Thesleff I.;
RT   "TNF signaling via the ligand-receptor pair ectodysplasin and edar
RT   controls the function of epithelial signaling centers and is
RT   regulated by Wnt and activin during tooth organogenesis.";
RL   Dev. Biol. 229:443-455(2001).
CC   -!- FUNCTION: Receptor for EDA isoform TAA, but not for EDA isoform
CC       TA-2 (By similarity). May mediate the activation of NF-kappa-B and
CC       JNK. May promote caspase-independent cell death.
CC   -!- SUBUNIT: Binds to EDARADD. Associates with TRAF1, TRAF2, TRAF3 and
CC       NIK.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- DEVELOPMENTAL STAGE: Transcripts are not detectable in the
CC       branchial arch epithelium before morphological tooth formation
CC       (E10), but are highly expressed during the initiation of tooth
CC       development (E11). Starting E12 expresssion is high and limited to
CC       the budding cells, and remains high in the fully developed enamel
CC       knot at E14, whereas all other dental cells were completely
CC       negative. During E15 the enamel knot disappears largely through
CC       apoptosis, and no transcripts were detected in the tooth germs of
CC       newborns. In skin, uniformly distributed in the basal cells of the
CC       epidermis before follicle initiation. Expression becomes focally
CC       elevated before placodes become distinguishable. By E17
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CC       transcripts are almost exclusively confined to maturing follicles
CC       and the recently initiated placodes.
CC   -!- INDUCTION: By activin A in E12 dental epithelium.
CC   -!- DISEASE: Defects in EDAR are a cause of the downless phenotype in
CC       mice (the equivalent of anhidrotic ectodermal dysplasia in
CC       humans). The disease is characterized by sparse hair (atrichosis
CC       or hypotrichosis), abnormal or missing teeth and the inability to
CC       sweat due to the absence of sweat glands.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF160502; AAD50425.1; -.
DR   EMBL; AK004576; BAB23385.1; ALT_INIT.
DR   MGD; MGI:1343498; Edar.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Receptor; Developmental protein; Differentiation; Apoptosis;
KW   Disease mutation; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1    26       POTENTIAL.
FT   CHAIN       27   448       TUMOR NECROSIS FACTOR RECEPTOR
FT                              SUPERFAMILY MEMBER EDAR.
FT   DOMAIN      27   187       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   188   208       POTENTIAL.
FT   DOMAIN     209   448       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     358   431       DEATH.
FT   REPEAT      30    71       TNFR-CYS 1.
FT   REPEAT      73   113       TNFR-CYS 2.
FT   REPEAT     115   150       TNFR-CYS 3.
FT   DISULFID    31    44       BY SIMILARITY.
FT   DISULFID    47    60       BY SIMILARITY.
FT   DISULFID    50    71       BY SIMILARITY.
FT   DISULFID    74    87       BY SIMILARITY.
FT   DISULFID    93   113       BY SIMILARITY.
FT   DISULFID   135   148       POTENTIAL.
FT   CARBOHYD    38    38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    379   379       E -> K (IN RECESSIVE DOWNLESS JACKSON).
SQ   SEQUENCE   448 AA;  48434 MW;  FCCAF38F3D6BB971 CRC64;

  Query Match             8.8%;  Score 198;  DB 1;  Length 448;
  Best Local Similarity   28.2%;  Pred. No. 8.1e-08;
  Matches   61;  Conservative   32;  Mismatches   83;  Indels   40;  Gaps   11;

Qy         16 LLVLLGYLSCKVTCESGDCRQQEFRDR-SGNCVPCNQCGPGMELSKECGFG-YGEDAQCV 73
              | ||:  | |    |  :| : |: :: :| |  |  | || |    ||:|   :|  ||
Db         13 LPVLVVSLMCSAKAEDSNCGENEYHNQTTGLCQQCPPCRPGEEPYMSCGYGTKDDDYGCV 72

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANC----SATSDAICGDCLPGFY----RKT 125
                |   :| :  |:| |:   ||      | :|         :|| || ||||:|    |
Db         73 PCPAEKFSKG-GYQICRRHKDC---EGFFRATVLTPGDMENDAECGPCLPGYYMLENRPR 128

Qy        126 KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTA--------------L 170
              : |   | | |    ||    |    : |   |:::|   |                |
Db        129 NIYG---MVCYSC-LLAPPNTKECVGATSGVSAHSSSTSGGSTLSPFQHAHKELSGQGHL 184

Qy        171 AAVICSALATVL---LALLILCVIYCKRQFMEKKPS 203
              |  :  |::|:    :|:::: : |     |: |||
Db        185 ATALIIAMSTIFIMAIAIVLIIMFY----IMKTKPS 216


RESULT 5
EDAR_HUMAN
ID   EDAR_HUMAN     STANDARD;      PRT;   448 AA.
AC   Q9UNE0; Q9UND9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member EDAR precursor
DE   (Anhidrotic ectodysplasin receptor 1) (Ectodysplasin-A receptor) (EDA-
DE   A1 receptor) (Ectodermal dysplasia receptor) (Downless homolog).
GN   EDAR OR DL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANTS HED ARG-87; HIS-89 AND GLN-420.
RC   TISSUE=Fetal heart, and Skin;
RX   MEDLINE=99364416; PubMed=10431241;
RA   Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA   Zonana J.;
RT   "Mutations in the human homologue of mouse dl cause autosomal
RT   recessive and dominant hypohidrotic ectodermal dysplasia.";
RL   Nat. Genet. 22:366-369(1999).
RN   [2]
RP   CHARACTERIZATION OF VARIANT GLN-420, MUTAGENESIS OF GLU-379,
RP   CHARACTERIZATION, AND INTERACTION WITH TRAF1 AND TRAF3.
RX   MEDLINE=21264720; PubMed=11035039;
RA   Kumar A., Eby M.T., Sinha S., Jasmin A., Chaudhary P.M.;
RT   "The ectodermal dysplasia receptor activates the nuclear
RT   factor-kappaB, JNK, and cell death pathways and binds to
RT   ectodysplasin A.";
RL   J. Biol. Chem. 276:2668-2677(2001).
RN   [3]
RP   EDA ISOFORM A1 BINDING.
RX   MEDLINE=20495245; PubMed=11039935;
RA   Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA   de Vos A.M., Gao W.-Q., Dixit V.M.;
RT   "Two-amino acid molecular switch in an epithelial morphogen that
RT   regulates binding to two distinct receptors.";
RL   Science 290:523-527(2000).
CC   -!- FUNCTION: Receptor for EDA isoform A1, but not for EDA isoform A2.
CC       Mediates the activation of NF-kappa-B and JNK. May promote
CC       caspase-independent cell death.
CC   -!- SUBUNIT: Binds to EDARADD. Associates with TRAF1, TRAF2, TRAF3 and
CC       NIK.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Detected in fetal kidney, lung, skin and
CC       cultured neonatal epidermal keratinocytes. Not detected in
CC       lymphoblast and fibroblast cell lines.
CC   -!- DEVELOPMENTAL STAGE: Found in craniofacial tissues from embryonic
CC       day 42-53. Expressed in fetal skin 11 and 15 weeks after
CC       gestation.
CC   -!- DISEASE: Defects in EDAR are a cause of autosomal recessive and
CC       dominant anhidrotic (hypohidrotic) ectodermal dysplasia (HED or
CC       EDA), a disease characterized by sparse hair (atrichosis or
CC       hypotrichosis), abnormal or missing teeth and the inability to
CC       sweat due to the absence of sweat glands.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF130988; AAD50076.1; -.
DR   EMBL; AF130996; AAD50077.1; -.
DR   EMBL; AF130990; AAD50077.1; JOINED.
DR   EMBL; AF130991; AAD50077.1; JOINED.
DR   EMBL; AF130992; AAD50077.1; JOINED.
DR   EMBL; AF130993; AAD50077.1; JOINED.
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DR   EMBL; AF130994; AAD50077.1; JOINED.
DR   EMBL; AF130995; AAD50077.1; JOINED.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:2895; EDAR.
DR   MIM; 604095; -.
DR   MIM; 224900; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; NAS.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Receptor; Developmental protein; Differentiation; Apoptosis;
KW   Disease mutation; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Anhidrotic ectodermal dysplasia.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    448       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER EDAR.
FT   DOMAIN       27    187       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    188    208       POTENTIAL.
FT   DOMAIN      209    448       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      358    431       DEATH.
FT   REPEAT       30     71       TNFR-CYS 1.
FT   REPEAT       73    113       TNFR-CYS 2.
FT   REPEAT      115    148       TNFR-CYS 3.
FT   DISULFID     31     44       BY SIMILARITY.
FT   DISULFID     47     60       BY SIMILARITY.
FT   DISULFID     50     71       BY SIMILARITY.
FT   DISULFID     74     87       BY SIMILARITY.
FT   DISULFID     93    113       BY SIMILARITY.
FT   DISULFID    135    148       BY SIMILARITY.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      87     87       C -> R (IN AUTOSOMAL RECESSIVE HED).
FT                                 /FTId=VAR_013448.
FT   VARIANT      89     89       R -> H (IN AUTOSOMAL RECESSIVE HED).
FT                                 /FTId=VAR_013449.
FT   VARIANT     420    420       R -> Q (IN AUTOSOMAL DOMINANT HED;
FT                                 ABOLISHES NF-KAPPA-B ACTIVATION AND
FT                                 REDUCES JNK ACTIVATION).
FT                                 /FTId=VAR_013450.
FT   MUTAGEN     379    379       E->K: REDUCES ACTIVATION OF NF-KAPPA-B.
FT   CONFLICT    262    262       P -> S (IN REF. 1).
SQ   SEQUENCE   448 AA;  48582 MW;  AC8D61249D608439 CRC64;

  Query Match             8.5%;  Score 191;  DB 1;  Length 448;
  Best Local Similarity   28.7%;  Pred. No. 2.7e-07;
  Matches   62;  Conservative   30;  Mismatches   84;  Indels   40;  Gaps   12;

Qy         16 LLVLLGYLSCKVTCESGDCRQQEFRDR-SGNCVPCNQCGPGMELSKECGFG-YGEDAQCV 73
              | ||:  | |     |  :| : |: :: :| |  |  ||||  |    ||:|   ||  ||
Db         13 LPVLVVSLMCSARAEYSNCGENEYYNQTTGLCQECPPCGPGEEPYLSCGYGTKDEDYGCV 72

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANC----SATSDAICGDCLPGFY----RKT 125
               |   :| :  |:| |:   ||     | :|         :|| || ||||:|    |
Db         73 PCPAEKFSKG-GYQICRRHKDC---EGFFRATVLTPGDMENDAECGPCLPGYYMLENRPR 128

Qy        126 KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKI------ASTASSPRDTA---------L 170
              : |   | |  |    ||    |   :           |: ||   |          |
Db        129 NIYG---MVCYSC-LLAPPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKELSGQGHL 184

Qy        171 AAVICSALATVL---LALLILCVIYCKRQFMEKKPS 203
              |  :  |::|:    :|:::: : |     :: |||
Db        185 ATALIIAMSTIFIMAIAIVLIIMFY----ILKTKPS 216


RESULT 6
EDAR_ORYLA
ID   EDAR_ORYLA     STANDARD;      PRT;   514 AA.
AC   Q90VY2; Q90Z36;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member EDAR precursor
DE   (Ectodysplasin-A receptor) (Reduced scale-3 protein).
GN   EDAR OR RS-3.
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AA2, and HNI;
RX   MEDLINE=21407746; PubMed=11516953;
RA   Kondo S., Kuwahara Y., Kondo M., Naruse K., Mitani H., Wakamatsu Y.,
RA   Ozato K., Asakawa S., Shimizu N., Shima A.;
RT   "The medaka rs-3 locus required for scale development encodes
RT   ectodysplasin-A receptor.";
RL   Curr. Biol. 11:1202-1206(2001).
CC   -!- FUNCTION: Receptor for EDA (By similarity). May mediate the
CC       activation of NF-kappa-B and JNK.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- DEVELOPMENTAL STAGE: Barely detectable on the body surface of 8
CC       and 15 day old fish. In 30 day old fish, when scale development
CC       has started, expression is high in patches of epithelial cell
CC       clusters and at the posterior margins of growing scales.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF364814; AAK83297.1; -.
DR   EMBL; AF364815; AAK83298.1; -.
DR   EMBL; AF364816; AAK83299.1; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Receptor; Developmental protein; Differentiation; Apoptosis;
KW   Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    514       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER EDAR.
FT   DOMAIN       28    183       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    184    204       POTENTIAL.
FT   DOMAIN      205    514       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      403    476       DEATH.
FT   REPEAT       31     72       TNFR-CYS 1.
FT   REPEAT       74    114       TNFR-CYS 2.
FT   REPEAT      116    149       TNFR-CYS 3.
FT   DISULFID     32     45       BY SIMILARITY.
FT   DISULFID     48     61       BY SIMILARITY.
FT   DISULFID     51     72       BY SIMILARITY.
FT   DISULFID     75     88       BY SIMILARITY.
FT   DISULFID     94    114       BY SIMILARITY.
FT   DISULFID    117    136       BY SIMILARITY.
FT   DISULFID    139    149       BY SIMILARITY.
FT   CARBOHYD     39     39       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      13     13       M -> V (IN STRAIN HNI).
FT   VARIANT     155    155       A -> P (IN STRAIN HNI).
FT   VARIANT     353    353       S -> T (IN STRAIN HNI).
SQ   SEQUENCE   514 AA;  56066 MW;  82C7F0661EECFB48 CRC64;

  Query Match             8.2%;  Score 185;  DB 1;  Length 514;
```

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  Best Local Similarity   24.8%;  Pred. No. 9.2e-07;
  Matches   63;  Conservative   37;  Mismatches   82;  Indels   72;  Gaps   14;

Qy          9 QEKTFF--TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFG 65
              |:|: |  :|||   : |     |   | : || ::: | |  | || || | :  || |
Db          9 QKKSMFLSSLLVCCMFAS----AEYSSCGEYEFFNQTSNSCQACPQCRPGQEPNMSCGHG 64

Qy         66 YGEDA-QCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANC----SATSDAICGDCLPG 120
                ::   ||| |  :: :   :: |:   ||   |   ||      :|  || || ||||
Db         65 MKDEGFACVPCPQGKYSKG-KYEICRRHKDC---NALYKATVREPGTAEKDAECGPCLPG 120

Qy        121 FYR-KTKLVGFQDMECVPCGDPP--------------PPYEPHCASKVNLVKIASTASS 164
               :|  : :      | |  | : |              ||  |   :      :     |
Db        121 YYMLENRARNLYAMVCHSCQNAPLNTKECKKTTEAIIKPPINPGSTT------VLPHPGS 174

Qy        165 PRDTALAAVICSALATVL---LALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCF 221
              |    ||  :  |::|:    :|:::: : |     :: ||             ||
Db        175 PGQGHLATALIIAMSTIFIMAIAIVLIIMFY----ILKAKP----------NG------ 213

Qy        222 DRPQLHEYAHRACC 235
                  :|||
Db        214 ----------QACC 217


RESULT 7
TR1A_MOUSE
ID   TR1A_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Bebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   EMBL; BC004599; AAH04599.1; -.
DR   PIR; A38634; GQMST1.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
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DR   GO; GO:0006952; P:defense response; IMP.
DR   GO; GO:0006954; P:inflammatory response; IMP.
DR   GO; GO:0007515; P:lymph gland development; IMP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      339    349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      356    441       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    185    191       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  0710C2E8C3C2B6D9 CRC64;

  Query Match             7.0%;  Score 157;  DB 1;  Length 454;
  Best Local Similarity  21.0%;  Pred. No. 0.00011;
  Matches   76;  Conservative   42;  Mismatches  140;  Indels  104;  Gaps   19;

Qy        34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGF-QKCKPC 92
             | | ::     | : | :|  |  |  :|    | |  |  |    |     : ::|  |
Db        44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCP-SPGRDTVCRECEKGTFTASQNYLRQCLSC 102

Qy        93 LDC-AVVNRFQKANCSATSDAICG-----------------DCLPGFYRKTKL------ 127
               |   ::: : : | |  | :||                 || | |     :
Db       103 KTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKETQ 162

Qy       128 -------VGF--QDMECVPCGDPPPPYEPHCASKVNLVKIA-----STASSPRDTALAAV 173
                    ||  :: |||||          ||      :|:      :  ::|:|:  | :
Db       163 NTVCNCHAGFFLRESECVPCS--------HCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214

Qy       174 ICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRA 233
             :      :|| | :|  |:     | : | |                   ||:::
Db       215 L---PLVILLGLCLLSFIFI--SLMCRYPRW-----------------RPEVYSII--- 248

Qy       234 CCQCRRDSV----QTCG-PVRLLPSMCCEEACSPNPATLGCGVHSAASLQARN------- 281
               | || |  .  :  | |:   ||          || |||      :|  :
Db       249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSPTSGFNP-TLGFSTPGFSSPVSSTPISPIFG 303

Qy       282 ------AGPAGEMVPTFFGS--LTQSICG----EFSDAWPLMQNPMGGDNISFCDSYPEL 329
                   |  |:|||      | :|:|          |    :|   ||       |  :
Db       304 PSNWHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWEDSAHPQRPDNADLAILYAVV 363

Qy       330 TG 331
               |
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Db        364 DG 365


RESULT 8
TR16_CHICK
ID   TR16_CHICK     STANDARD;      PRT;   416 AA.
AC   P18519;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE   (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSF16.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90166579; PubMed=2560385;
RA   Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
RA   Shooter E.M., Reichardt L.F.;
RT   "Structure and developmental expression of the nerve growth factor
RT   receptor in the chicken central nervous system.";
RL   Neuron 2:1123-1134(1989).
RN   [2]
RP   SEQUENCE OF 21-416 FROM N.A.
RX   MEDLINE=90152140; PubMed=2154393;
RA   Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT   "Structure and developmental expression of the chicken NGF receptor.";
RL   Dev. Biol. 137:287-304(1990).
CC   -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC       and NT-4. Can mediate cell survival as well as cell death of
CC       neural cells (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC       associated cell death executor. Interacts with TRAF2, TRAF4 and
CC       TRAF6 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: N- AND O-glycosylated.
CC   -!- PTM: Phosphorylated on serine residues.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
DR   PIR; JN0006; JN0006.
DR   HSSP; P07174; 1NGR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW   Repeat; Phosphorylation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    416       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 16.
FT   DOMAIN       29    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    240    261       POTENTIAL.
FT   DOMAIN      262    416       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       23     57       TNFR-CYS 1.
FT   REPEAT       58     99       TNFR-CYS 2.
FT   REPEAT      100    138       TNFR-CYS 3.
FT   REPEAT      140    180       TNFR-CYS 4.
FT   DOMAIN      333    410       DEATH.
FT   DOMAIN      188    236       SER/THR-RICH.
FT   DISULFID     24     35       BY SIMILARITY.
FT   DISULFID     36     49       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
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FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID     78     91       BY SIMILARITY.
FT   DISULFID     81     99       BY SIMILARITY.
FT   DISULFID    101    114       BY SIMILARITY.
FT   DISULFID    117    130       BY SIMILARITY.
FT   DISULFID    120    138       BY SIMILARITY.
FT   DISULFID    141    156       BY SIMILARITY.
FT   DISULFID    159    172       BY SIMILARITY.
FT   DISULFID    162    180       BY SIMILARITY.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     36     36       C -> Y (IN REF. 2).
FT   CONFLICT    173    173       T -> K (IN REF. 2).
FT   CONFLICT    276    276       N -> S (IN REF. 2).
FT   CONFLICT    396    396       K -> R (IN REF. 2).
SQ   SEQUENCE   416 AA;  44654 MW;  6BCEAAB54F4D2D56 CRC64;

  Query Match             6.6%;  Score 148;  DB 1;  Length 416;
  Best Local Similarity   31.0%;  Pred. No. 0.00046;
  Matches   58;  Conservative   17;  Mismatches   80;  Indels   32;  Gaps   11;

Qy         20 LGYLSCKVTC-ESGD----CRQQEFRDR-SGNCVPCNQCGPGMELSKECGFGY------G 67
              :|  |    | || |    |    |:|  ||:|  |: |         | |||
Db         82 VGLHSMSAPCVESDDAVCRCAYGYFQDELSGSCKECSIC--------EVGFGLMFPCRDS 133

Qy         68 EDAQCVTCRLHRFKEDWGFQKCKPCLDCAVV--NRFQKANCSATSDAICGDCLPGFYRKT 125
              :|  |  |    | ::  |    |||| :  |      |:|||| | |  | :   |
Db        134 QDTVCEECPEGTFSDEANF--VDPCLPCTICEENEVMVKECTATSDAECRDLHPRWTTHT 191

Qy        126 -KLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSP---RDTA--LAAVICSALA 179
               |  |    |  |    |  |    :  ::|    :| |   | ||  |  | || ||
Db        192 PSLAGSDSPE--PITRDPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPVYCSILA 249

Qy        180 TVLLALL 186
               |:: |:
Db        250 AVVVGLV 256


RESULT 9
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE   protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99223511; PubMed=10207006;
RA   Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT   "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT   death in HeLa cells.";
RL   J. Biol. Chem. 274:11868-11873(1999).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20261554; PubMed=10799510;
RA   Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA   Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT   "The lymphotoxin-beta receptor is necessary and sufficient for
RT   LIGHT-mediated apoptosis of tumor cells.";
RL   J. Biol. Chem. 275:14307-14315(2000).
RN   [6]
RP   INTERACTION WITH TRAF3.
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
RN   [7]
RP   INTERACTION WITH TRAF4.
RX   PubMed=9626059;
RA   Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA   Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,
RA   Reynolds A., Clevenger C.V., Reed J.C.;
RT   "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT   adult, fetal, and tumor tissues.";
RL   Am. J. Pathol. 152:1549-1561(1998).
RN   [8]
RP   INTERACTION WITH TRAF5.
RX   MEDLINE=98172745; PubMed=9511754;
RA   Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA   Otsuka M., Yamamoto T., Inoue J.-I.;
RT   "Cloning and characterization of a cDNA encoding the human homolog of
RT   tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL   Gene 207:135-140(1998).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs.
CC   -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; L04270; AAA36757.1; -.
DR   EMBL; BC026262; AAH26262.1; -.
DR   PIR; I54182; I54182.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:6718; LTBR.
DR   MIM; 600979; -.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1    30       POTENTIAL.
FT   CHAIN       31   435       TUMOR NECROSIS FACTOR RECEPTOR
FT                              SUPERFAMILY MEMBER 3.
FT   DOMAIN      31   227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   228   248       POTENTIAL.
FT   DOMAIN     249   435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42    81       TNFR-CYS 1.
FT   REPEAT      82   124       TNFR-CYS 2.
FT   REPEAT     125   168       TNFR-CYS 3.
FT   REPEAT     169   211       TNFR-CYS 4.
FT   DISULFID    43    58       BY SIMILARITY.
FT   DISULFID    59    72       BY SIMILARITY.
FT   DISULFID    62    80       BY SIMILARITY.
FT   DISULFID    83    98       BY SIMILARITY.
FT   DISULFID   101   116       BY SIMILARITY.
FT   DISULFID   104   124       BY SIMILARITY.
FT   DISULFID   126   132       BY SIMILARITY.
FT   DISULFID   139   148       BY SIMILARITY.
FT   DISULFID   142   167       BY SIMILARITY.
FT   DISULFID   170   185       BY SIMILARITY.
FT   CARBOHYD    40    40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177   177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match             6.5%;  Score 146.5;  DB 1;  Length 435;
  Best Local Similarity   21.4%;  Pred. No. 0.00063;
  Matches   73;  Conservative   42;  Mismatches  107;  Indels  119;  Gaps   19;

Qy         16 LLVLLGYLSCK-------VTCESGDCRQQE---FRDRSGNCVPCNQCGPGMELSKECGFG 65
              :| | | |:           |:  || ||   :  :   |  |::| ||  :| :|
Db         18 VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQHRIC--CSRCPPGTYVSAKC--S 73

Qy         66 YGEDAQCVTCRLHRFKEDWGF----QKCKPC------LDCAVVNRFQKANCSATSDAIC- 114
                | | ||  : : | | :     | |:||       : |     :|  |        |
Db         74 RIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCA 133

Qy        115 ------------GDCLPGFYRKTK-LVGFQDMECVPC--------GDPPPPYEPH--CAS 151
                         || ||   : |  ||  :  ||||           |    :||  | :
Db        134 AWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCEN 193

Qy        152 KVNLVKIA-------STASSPRD--------TALAAVICSALATVLLALLILCVIY---- 192
              :  ||: |        :|  :| :         | |   :   ||  ||   :   |:
Db        194 Q-GLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLMLAVLLPLAFFLLLATVFSCIWKSHP 252

Qy        193 --CKR--QFMEKKP----------SWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCR 238
                |::    ::::|          ||                : |: | |
Db        253 SLCRKLGSLLKRRPQGEGPNPVAGSW----------------EPPKAHPYF-------- 287

Qy        239 RDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQA 279
               | ||   |:           | : : :  |: :|  |:|
Db        288 PDLVQPLLPI-----------SGDVSPVSTGLPAAPVLEA 316


RESULT 10
TNR4_RAT
ID   TNR4_RAT       STANDARD;      PRT;   271 AA.
AC   P15725;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE   receptor) (OX40 antigen) (MRC OX40).
GN   TNFRSF4 OR TXGP1L OR OX40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=T-cell;
RX   MEDLINE=90214614; PubMed=2157591;
RA   Mallett S., Fossum S., Barclay A.N.;
RT   "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT   lymphocytes -- a molecule related to nerve growth factor receptor.";
RL   EMBO J. 9:1063-1068(1990).
CC   -!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
CC   -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X17037; CAA34897.1; -.
DR   PIR; S12783; S12783.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1    19       POTENTIAL.
FT   CHAIN       20   271       TUMOR NECROSIS FACTOR RECEPTOR
FT                              SUPERFAMILY MEMBER 4.
FT   DOMAIN      20   210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211   235       POTENTIAL.
FT   DOMAIN     236   271       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      25    60       TNFR-CYS 1.
FT   REPEAT      61   102       TNFR-CYS 2.
FT   REPEAT     103   123       TNFR-CYS 3 (INCOMPLETE).
FT   REPEAT     124   164       TNFR-CYS 4.
FT   DISULFID    26    37       BY SIMILARITY.
FT   DISULFID    38    51       BY SIMILARITY.
FT   DISULFID    41    59       BY SIMILARITY.
FT   DISULFID    62    76       BY SIMILARITY.
FT   DISULFID    79    94       BY SIMILARITY.
FT   DISULFID    82   102       BY SIMILARITY.
FT   DISULFID   104   122       BY SIMILARITY.
FT   DISULFID   125   138       BY SIMILARITY.
FT   DISULFID   144   163       BY SIMILARITY.
FT   CARBOHYD   143   143       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   271 AA;  29895 MW;  C06465136B16E821 CRC64;

  Query Match             6.4%;  Score 145;  DB 1;  Length 271;
  Best Local Similarity   29.8%;  Pred. No. 0.00047;
  Matches   57;  Conservative   19;  Mismatches   75;  Indels   40;  Gaps   13;

Qy          9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG 63
              |: | | || | ||    |:| | |  ||             |  | :| ||  :   |
Db          6 QQPTAFLLLGLSLGVTVKLNCVKDTYPSGH----------KC--CRECQPGHGMVSRC- 51

Qy         64 FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFY 122
               :  |  |  |    : |   :  || |  |   :  : | ||: | | :|  | ||
Db         52 -DHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQ 109

Qy        123 RKTKLVGFQDMECVPCGDPPPPYEP----HCASKVNLV----KIASTASSPRDTALAAVI 174
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              :        ::||||  ||  : |     |    |      :|   ||:  ||     :
Db        110 PRQDSSHKLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy        175 C---SALATVL 182
              |   | |||:|
Db        163 CEDRSLLATLL 173


RESULT 11
TNR4_MOUSE
ID   TNR4_MOUSE     STANDARD;      PRT;   272 AA.
AC   P47741;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE   receptor) (OX40 antigen).
GN   TNFRSF4 OR TXGP1 OR OX40.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=94044750; PubMed=8228223;
RA   Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA   Claassen E., Noelle R.J., Fell H.;
RT   "Cloning of mouse Ox40: a T cell activation marker that may mediate
RT   T-B cell interactions.";
RL   J. Immunol. 151:5261-5271(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95255413; PubMed=7737295;
RA   Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Barclay A.N.;
RT   "Gene structure and chromosomal localization of the mouse homologue
RT   of rat OX40 protein.";
RL   Eur. J. Immunol. 25:926-930(1995).
CC   -!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
CC   -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z21674; CAA79772.1; -.
DR   EMBL; X85214; CAA59476.1; -.
DR   PIR; I48700; I48700.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:104512; Tnfrsf4.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0006968; P:cellular defense response; IMP.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    272       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 4.
FT   DOMAIN       20    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    236       POTENTIAL.
FT   DOMAIN      237    272       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       26     61       TNFR-CYS 1.
FT   REPEAT       62    103       TNFR-CYS 2.
FT   REPEAT      104    124       TNFR-CYS 3 (INCOMPLETE).
FT   REPEAT      125    165       TNFR-CYS 4.
FT   DISULFID     27     38       BY SIMILARITY.
FT   DISULFID     39     52       BY SIMILARITY.
FT   DISULFID     42     60       BY SIMILARITY.
FT   DISULFID     63     77       BY SIMILARITY.
FT   DISULFID     80     95       BY SIMILARITY.
FT   DISULFID     83    103       BY SIMILARITY.
FT   DISULFID    105    123       BY SIMILARITY.
FT   DISULFID    126    139       BY SIMILARITY.
FT   DISULFID    145    164       BY SIMILARITY.
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     15     15       A -> G (IN REF. 2).
SQ   SEQUENCE   272 AA;  30153 MW;  06E7BB4156F0D08E CRC64;

  Query Match             6.4%;  Score 144;  DB 1;  Length 272;
  Best Local Similarity   29.5%;  Pred. No. 0.00056;
  Matches   54;  Conservative   21;  Mismatches   76;  Indels   32;  Gaps   13;

Qy         15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGN-CVPCNQCGPGMELSKECGFGYGEDAQCV 73
              | |:||  |:  ||    :| :  :   ||: |  | :| ||  :   |   :  |  |
Db          9 TALLLLA-LTLGVTARRLNCVKHTY--PSGHKC--CRECQPGHGMVSRC--DHTRDTLCH 61

Qy         74 TCRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQD 132
               |    : |   :  || |  |   :  : | ||: | | :|  | ||   :       ||
Db         62 PCETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPR------QD 114

Qy        133 ------MECVPCGDPPPPYEP----HCASKVNLVKIASTASSPRDTALAAVIC---SALA 179
                   ::||||  ||  : |     |    |           |   :| || |   | ||
Db        115 SGYKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171

Qy        180 TVL 182
              |:|
Db        172 TLL 174


RESULT 12
LMB2_RAT
ID   LMB2_RAT       STANDARD;      PRT;  1801 AA.
AC   P15800;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN   LAMB2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89159410; PubMed=2922051;
RA   Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT   "A laminin-like adhesive protein concentrated in the synaptic cleft
RT   of the neuromuscular junction.";
RL   Nature 338:229-234(1989).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration, and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       Comprising one long and three short arms with globules at each
CC       end.
CC       THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC       (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC       COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CC       CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC   -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
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CC       WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC   -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   -!- SIMILARITY: Contains 13 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 1 laminin IV domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X16563; CAA34561.1; -.
DR   PIR; S03539; MMRTS.
DR   HSSP; P02468; 1KLO.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001886; LamNT.
DR   Pfam; PF00053; laminin_EGF; 13.
DR   Pfam; PF00055; laminin_Nterm; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00180; EGF_Lam; 13.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00022; EGF_1; 10.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW   Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW   Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT   SIGNAL       1     35
FT   CHAIN       36   1801       LAMININ BETA-2 CHAIN.
FT   DOMAIN      36    283       LAMININ N-TERMINAL (DOMAIN VI).
FT   DOMAIN     286    349       LAMININ EGF-LIKE 1.
FT   DOMAIN     350    412       LAMININ EGF-LIKE 2.
FT   DOMAIN     413    472       LAMININ EGF-LIKE 3.
FT   DOMAIN     473    524       LAMININ EGF-LIKE 4.
FT   DOMAIN     525    555       LAMININ EGF-LIKE 5 (INCOMPLETE).
FT   DOMAIN     556    785       LAMININ DOMAIN IV.
FT   DOMAIN     786    833       LAMININ EGF-LIKE 6.
FT   DOMAIN     834    879       LAMININ EGF-LIKE 7.
FT   DOMAIN     880    929       LAMININ EGF-LIKE 8.
FT   DOMAIN     930    988       LAMININ EGF-LIKE 9.
FT   DOMAIN     989   1040       LAMININ EGF-LIKE 10.
FT   DOMAIN    1041   1097       LAMININ EGF-LIKE 11.
FT   DOMAIN    1098   1145       LAMININ EGF-LIKE 12.
FT   DOMAIN    1146   1192       LAMININ EGF-LIKE 13.
FT   DOMAIN    1193   1412       DOMAIN II.
FT   DOMAIN    1413   1445       DOMAIN ALPHA.
FT   DOMAIN    1446   1801       DOMAIN I.
FT   DOMAIN    1259   1306       COILED COIL (POTENTIAL).
FT   DOMAIN    1475   1529       COILED COIL (POTENTIAL).
FT   DOMAIN    1576   1793       COILED COIL (POTENTIAL).
FT   DISULFID   286    295       BY SIMILARITY.
FT   DISULFID   288    313       BY SIMILARITY.
FT   DISULFID   315    324       BY SIMILARITY.
FT   DISULFID   327    347       BY SIMILARITY.
FT   DISULFID   350    359       BY SIMILARITY.
FT   DISULFID   352    377       BY SIMILARITY.
FT   DISULFID   380    389       BY SIMILARITY.
FT   DISULFID   392    410       BY SIMILARITY.
FT   DISULFID   413    426       BY SIMILARITY.
FT   DISULFID   415    441       BY SIMILARITY.
FT   DISULFID   443    452       BY SIMILARITY.
FT   DISULFID   455    470       BY SIMILARITY.
FT   DISULFID   473    487       BY SIMILARITY.
FT   DISULFID   475    494       BY SIMILARITY.
FT   DISULFID   496    505       BY SIMILARITY.
FT   DISULFID   508    522       BY SIMILARITY.
FT   DISULFID   786    798       BY SIMILARITY.
FT   DISULFID   788    805       BY SIMILARITY.
FT   DISULFID   807    816       BY SIMILARITY.
FT   DISULFID   819    831       BY SIMILARITY.
FT   DISULFID   834    846       BY SIMILARITY.
FT   DISULFID   836    853       BY SIMILARITY.
FT   DISULFID   855    864       BY SIMILARITY.
FT   DISULFID   867    877       BY SIMILARITY.
FT   DISULFID   880    889       BY SIMILARITY.
FT   DISULFID   882    896       BY SIMILARITY.
FT   DISULFID   899    908       BY SIMILARITY.
FT   DISULFID   911    927       BY SIMILARITY.
FT   DISULFID   930    946       BY SIMILARITY.
FT   DISULFID   932    957       BY SIMILARITY.
FT   DISULFID   959    968       BY SIMILARITY.
FT   DISULFID   971    986       BY SIMILARITY.
FT   DISULFID   989   1003       BY SIMILARITY.
FT   DISULFID   991   1010       BY SIMILARITY.
FT   DISULFID  1013   1022       BY SIMILARITY.
FT   DISULFID  1025   1038       BY SIMILARITY.
FT   DISULFID  1098   1110       BY SIMILARITY.
FT   DISULFID  1100   1117       BY SIMILARITY.
FT   DISULFID  1119   1128       BY SIMILARITY.
FT   DISULFID  1131   1143       BY SIMILARITY.
FT   DISULFID  1146   1158       BY SIMILARITY.
FT   DISULFID  1148   1165       BY SIMILARITY.
FT   DISULFID  1167   1176       BY SIMILARITY.
FT   DISULFID  1179   1190       BY SIMILARITY.
FT   DISULFID  1193   1193       INTERCHAIN (PROBABLE).
FT   DISULFID  1196   1196       INTERCHAIN (PROBABLE).
FT   DISULFID  1800   1800       INTERCHAIN (PROBABLE).
FT   CARBOHYD   251    251       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   371    371       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1088   1088       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1252   1252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1311   1311       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1351   1351       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1502   1502       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1801 AA;  196473 MW;  97AEF32F8F31FA75 CRC64;

  Query Match             6.3%;  Score 142.5;  DB 1;  Length 1801;
  Best Local Similarity   22.6%;  Pred. No. 0.0067;
  Matches   98;  Conservative   33;  Mismatches  147;  Indels  155;  Gaps   27;

Qy         17 LVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKEC--------GFG--- 65
              ||  | | |:  |:       |     | |    :| ||: : : |       |||
Db        778 LVYNGALPCQ--CDPQGSLSSECNPHGGQC----RCKPGV-VGRRCDACATGYYGFGPAG 830

Qy         66 ----------------YGEDAQCVTCRLHRF--------KEDWGFQKCKPCLDCAVVNRF 101
                            |   ||: ||   |        :  |||   |:||     |
Db        831 CQACQCSPDGALSALCEGTSGQCL-CRTGAFGLRCDHCQRGQWGFPNCRPC-----VCNG 884

Qy        102 QKANCSATSDAI----------CGDCLPGFYRKTKL-VGFQDMECVPCGDPP-PPYEPH 148
              :   | | : |           |  |: ||:   :|  | |   | ||  |  | : |
Db        885 RADECDAHTGACLGCRDYTGGEHCERCIAGFHGDPRLPYGGQ---CRPCPCPEGPGSQRH 941

Qy        149 CASKVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFME-KKPSWSLR 207
               |:          | ||     ::|   |       : |       | :  ||    :
Db        942 FAT----------SCHRDGYSQQIVCHCRAGY---TGLRCEACAPGHFGDPSKPGGRCQ 987

Qy        208 ----SQDIQ---------YNGSELSCFD----------RPQLHEYA-----HRACCQCRR 239
                  | :|          : |  | |           :|  |  |      ||  |
Db        988 LCECSGNIDPTDPGACDPHTGQCLRCLHHTEGPHCGHCKPGFHGQAARQSCHRCTCNLLG 1047

Qy        240 DSVQTC-----------GPVRLLP---SMCCEEACSPN--PATLGCGVHSAASLQARNA 282
                | |           |    ||    : |:  |:||    | | |    |   :|
Db       1048 TDPQRCPSTDLCHCDPSTGQCPCLPHVQGLSCDR-CAPNFWNFTSGRGCQPCACHPSRAR 1106

Qy        283 GP-----------AGEMVPTFFGSLTQSICGEFSDAWPLMQ------NPMGGD------ 318
              ||           ||      ||  | | | |     | :|      :| | |
Db       1107 GPTCNEFTGQCHCHAG------FGGRTCSECQELHWGDPGLQCRACDCDPRGIDKPQCHR 1160

Qy        319 NISFCDSYPELTG 331
              :   |   | ::|
Db       1161 STGHCSCRPGVSG 1173
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RESULT 13
NFX1_HUMAN
ID   NFX1_HUMAN      STANDARD;      PRT;  1104 AA.
AC   Q12986;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Transcriptional repressor NF-X1 (EC 6.3.2.-) (Nuclear transcription
DE   factor, X box-binding, 1).
GN   NFX1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95053707; PubMed=7964459;
RA   Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
RT   "A novel cysteine-rich sequence-specific DNA-binding protein
RT   interacts with the conserved X-box motif of the human major
RT   histocompatibility complex class II genes via a repeated Cys-His
RT   domain and functions as a transcriptional repressor.";
RL   J. Exp. Med. 180:1763-1774(1994).
RN   [2]
RP   FUNCTION AS A E2-DEPENDENT UBIQUITIN LIGASE.
RX   MEDLINE=99432238; PubMed=10500182;
RA   Lorick K.L., Jensen J.P., Fang S., Ong A.M., Hatakeyama S.,
RA   Weissman A.M.;
RT   "RING fingers mediate ubiquitin-conjugating enzyme (E2)-dependent
RT   ubiquitination.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:11364-11369(1999).
CC   -!- FUNCTION: Repressor of HLA-DRA transcription. Binds to the X-box
CC       motif of MHC class II genes. May play an important role in
CC       regulating the duration of an inflammatory response by limiting
CC       the period in which MHC class II molecules are induced by
CC       interferon-gamma. Mediates E2-dependent ubiquitation.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- INDUCTION: By interferon gamma.
CC   -!- DOMAIN: The RING-type zinc finger domain interacts with an
CC       ubiquitin-conjugating enzyme (E2) and facilitates ubiquititation.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 R3H domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U15306; AAA69517.1; -.
DR   PIR; I38869; I38869.
DR   TRANSFAC; T01694; -.
DR   Genew; HGNC:7803; NFX1.
DR   MIM; 603255; -.
DR   GO; GO:0003700; F:transcription factor activity; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR   GO; GO:0006366; P:transcription from Pol II promoter; TAS.
DR   InterPro; IPR001374; R3H.
DR   InterPro; IPR000967; Znf_NFX1.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF01424; R3H; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF01422; zf-NF-X1; 8.
DR   SMART; SM00393; R3H; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00438; ZnF_NFX; 9.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Ubl conjugation pathway; Ligase; Transcription regulation; Repressor;
KW   DNA-binding; Nuclear protein; Repeat; Zinc-finger.
FT   ZN_FING      342    393       RING-TYPE.
FT   DOMAIN       424    876       7 X APPROXIMATE REPEATS, CYS-RICH.
FT   REPEAT       424    463       1.
FT   REPEAT       480    517       2.
FT   REPEAT       541    580       3.
FT   REPEAT       606    647       4.
FT   REPEAT       695    734       5.
FT   REPEAT       806    842       6.
FT   REPEAT       843    876       7.
FT   DOMAIN       992   1041       R3H.
FT   DOMAIN      1068   1073       POLY-PRO.
SQ   SEQUENCE  1104 AA;  123149 MW;  36FEC4292F78130C CRC64;

  Query Match             6.3%;  Score 142;  DB 1;  Length 1104;
  Best Local Similarity   18.8%;  Pred. No. 0.0041;
  Matches  110;  Conservative   58;  Mismatches  182;  Indels  236;  Gaps   27;

Qy         24 SCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG-------FGYGEDAQC---- 72
              || : |  |                 ||  |    |  : |||         |      |
Db        440 SCNLLCHPG---------------PCPPCPAFMTKTCECGRTRHTVRCGQAVSVHCSNPC 484

Qy         73 ---VTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATS-DAICGDCLPGFYRKTKLV 128
                 : |  |:  |     :|:||    ::|  |   | :|| | :||  :       |
Db        485 ENILNCGQHQCAELCHGGQCQPCQ--IILN--QVCYCGSTSRDVLCGTDV------GKSD 534

Qy        129 GFQDMEC-------VPCGD--------PPP-------PYEPHC--ASKVNLVKIASTASS 164
              || |  |       : ||:         | |       |    |    :  | ::    ||
Db        535 GFGDFSCLKTCGKDLKCGNHTCSQVCHPQPCQQCPRLPQLVRCCPCGQTPLSQLLELGSS 594

Qy        165 PRDTALAAV-----IC-SALATVLLALLILC---------------VIYCKRQFMEKK- 201
              | | :  |     :|   |    |  :  |               || |:  |  |:
Db        595 SRKTCMDPVPSCGKVCGKPLPCGSLDFIHTCEKLCHEGDCGPVSRTSVISCRCSFRTKEL 654

Qy        202 PSWSLRSQDI--------------QYNGSELSCFDRPQ------------LH---EYA 230
              |  ||:|:|                ::  :|: | |:                ||   |
Db        655 PCTSLKSEDATFMCDKRCNKKRLCGRHKCNEICCVDKEHKCPLNCGRKLRCGLHRCEEPC 714

Qy        231 HRACCQ-CRRDSVQT----CGPVRLLPSMCC--------------------------EE 258
              ||  || | : |       ||   : | : |                          ||
Db        715 HRGNCQTCWQASFDELTCHCGASVIYPPVPCGTRPPECTQTCARVHECDHPVYHSGHSEE 774

Qy        259 ACS-----------------------------PNPATLGCGVHSAASL---------- 277
              |                             |  |||  ||:|    |
Db        775 KCPPCTFLTQKWCMGKHEFRSNIPCHLVDISCGLPCSATLPCGMHKCQRLCHKGECLVDE 834

Qy        278 --------------------------------QAR-----NAGPAGEMVPTFFGSLTQSI 300
                                             :|:       |   |||     | |
Db        835 PCKQPCTTPRADCGHPCMAPCHTSSPCPVTACKAKVELQCECGRRKEMVICSEASSTYQR 894

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
                | |  :   :||      :   :| :::|    | :   |      :  :   |
Db        895 IAAISMASKITDMQLGGS----VEISKLITKKEVHQARLECDEECSALERKKR--LAEAF 948

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAII 406
               :   |: |   :  |:::::| | |  :  |   | :::|   ::
Db        949 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 992


RESULT 14
TR1A_RAT
ID   TR1A_RAT       STANDARD;      PRT;   461 AA.
AC   P22934; Q91V30; Q91Y93;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC   STRAIN=BB(DR)/Wor, LEW/NHsd, ACI/SegHsd, DA/Bkl, F344/NHsd, and
RC   BN/SsNHsd;
RA   Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT   among autoimmune susceptible and resistant inbred rat strains.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC       homotrimerization. The aggregated death domains provide a novel
CC       molecular interface that interacts specifically with the death
CC       domain of TRADD. Various TRADD-interacting proteins such as TRAFS,
CC       RIP and possibly FADD, are recruited to the complex by their
CC       association with TRADD. This complex activates at least two
CC       distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC       Binds BAG4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   EMBL; AF329976; AAK53562.1; -.
DR   EMBL; AF329977; AAK53563.1; -.
DR   EMBL; AF329981; AAK53567.1; -.
DR   EMBL; AF329978; AAK53564.1; -.
DR   EMBL; AF329979; AAK53565.1; -.
DR   EMBL; AF329980; AAK53566.1; -.
DR   PIR; B36555; GQRTT1.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     363    448       DEATH.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    195       BY SIMILARITY.
FT   DISULFID   185    191       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    230    230       I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                               DA/BKL AND F344/NHSD).
FT   VARIANT    295    295       H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                               DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FBD202 CRC64;
```

```
  Query Match              6.3%;  Score 141.5;  DB 1;  Length 461;
  Best Local Similarity   21.6%;  Pred. No. 0.0016;
  Matches   72;  Conservative   37;  Mismatches  113;  Indels  111;  Gaps   20;

Qy         34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCL 93
              | | ::     | : | :|  |  |  :|    |::  |  |    |          : ||
Db         44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCP-SPGQETVCEVCDKGTFTASQ--NHVRQCL 100

Qy         94 DCAVVNR--FQK--ANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPC---------- 138
                |    :  ||   : | |  | :||   .| |      || ::| ||
Db        101 SCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKE 160

Qy        139 --------------GDPPPPYEPHCASKVNLVKI----ASTASSPRDTALAAVICSALA 179
                           |:  |  ||    :|:    :  ::|:|:  | ::   :
Db        161 KQNTVCNCHAGFFLSGNECTPCS-HCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIF 219

Qy        180 TVLLALLILCV-IYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCR 238
                 |  | :|: : |     : | |              ||:::         |
Db        220 LGLCLLFFICISLLC------RYPQW-----------------RPRVYSII------C- 248

Qy        239 RDSVQTCGPVR----------LLPSMCCEEACSPNPA---TLGCGV-----HSAASLQA 279
                 |||    ||:          | |:    | ||||   |||       |  :|
Db        249 RDS----APVKEVEGEGIVTKPLTPASI--PAFSPNPGFNPTLGFSTTPRFSHPVSSTPI 302

Qy        280 RNA-GPAG---------EMVPT------FFGSL 296
                 ||:          |:|||       :|||
Db        303 SPVFGPSNWHNFVPPVREVVPTQGADPLLYGSL 335
```

```
RESULT 15
TRLT_MACFA
ID   TRLT_MACFA     STANDARD;      PRT;   430 AA.
AC   Q9N092;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 19L precursor
DE   (Receptor expressed in lymphoid tissues).
GN   TNFRSF19L OR RELT.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21458551; PubMed=11574149;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
RA   Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kususda J.;
```

```
RT   "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT   chromosomes.";
RL   Gene 275:31-37(2001).
CC   -!- FUNCTION: Mediates activation of NF-kappa-B (By similarity). May
CC       play a role in T-cell activation.
CC   -!- SUBUNIT: Associates with TRAF1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB046039; BAB01621.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00208; TNFR; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    430       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 19L.
FT   DOMAIN       27    162       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    163    183       POTENTIAL.
FT   DOMAIN      184    430       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       50     90       TNFR-CYS.
FT   DISULFID     51     65       BY SIMILARITY.
FT   DISULFID     71     90       BY SIMILARITY.
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   430 AA;  45850 MW;  BA8DE92593E1E859 CRC64;

  Query Match             6.2%;  Score 141;  DB 1;  Length 430;
  Best Local Similarity   25.6%;  Pred. No. 0.0016;
  Matches   44;  Conservative   23;  Mismatches   57;  Indels   48;  Gaps    6;

Qy         51 QCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATS 110
              || ||    :|      |:   |  |    |   ||   |:|   |::  | :    :||
Db         31 QCPPG----EEPDLNPGQGTLCRPCPPGTFSAAWGSSPCQPHARCSLQRRLEAQVGTATQ 86

Qy        111 DAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNL-------------VK 157
              | :|||| ||::               | | |  | :|   : : :             |:
Db         87 DTLCGDCWPGWFG-------------PWGVPRVPCQPCSWAPLGIHGCDEWGRRARRGVE 133

Qy        158 IASTASS---------------PRDTALA-AVICSALATVLLALLILCVIYC 193
              :|: |||               | :||   |||  |:  |   : :| :: |
Db        134 VAAGASSGGETRQPGNGTRAGGPEETAAQYAVI--AIVPVFCLMGLLGILVC 183


Search completed: January 29, 2004, 21:39:07
Job time : 19 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:36:16 ; Search time 40 Seconds
(without alignments)
2690.198 Million cell updates/sec

Title: US-09-780-532A-2
Perfect score: 2256
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....LDQESGAIIHPATQTSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1559.5	69.1	416	11	Q8BUM7	Q8bum7 mus musculu
2	846.5	37.5	273	11	Q8BWR1	Q8bwr1 mus musculu
3	497	22.0	297	11	Q8BX35	Q8bx35 mus musculu
4	496	22.0	297	11	Q8BM50	Q8bm50 mus musculu
5	488	21.6	318	4	Q8IZA6	Q8iza6 homo sapien
6	486	21.5	185	11	Q8BJS6	Q8bjs6 mus musculu
7	172	7.6	387	13	Q9PVD4	Q9pvd4 xenopus lae
8	155	6.9	276	13	Q9DDD2	Q9ddd2 gallus gall
9	145	6.4	1024	4	Q9BXI1	Q9bxi1 homo sapien
10	142	6.3	1120	4	Q96EL5	Q96el5 homo sapien
11	141	6.2	436	11	Q8BTV0	Q8btv0 mus musculu
12	140.5	6.2	548	5	Q9GQ45	Q9gq45 giardia lam
13	139	6.2	317	13	Q8JFV6	Q8jfv6 brachydanio
14	138.5	6.1	186	12	O72735	O72735 cowpox viru
15	136.5	6.1	350	12	O57123	O57123 cowpox viru
16	136	6.0	401	13	Q9PRG7	Q9prg7 xenopus lae
17	136	6.0	417	11	Q8BYY1	Q8byy1 mus musculu
18	136	6.0	427	11	Q8CFT3	Q8cft3 mus musculu
19	135.5	6.0	2813	11	Q8CIZ8	Q8ciz8 mus musculu
20	135	6.0	186	12	Q9YP87	Q9yp87 cowpox viru
21	135	6.0	348	12	O57108	O57108 monkeypox v
22	135	6.0	348	12	O57277	O57277 monkeypox v
23	135	6.0	348	12	O57103	O57103 monkeypox v
24	134	5.9	436	11	Q8BX43	Q8bx43 mus musculu
25	133.5	5.9	3396	5	Q9VM55	Q9vm55 drosophila
26	133	5.9	1650	11	Q9QVT6	Q9qvt6 rattus sp.
27	132.5	5.9	349	12	O57100	O57100 monkeypox v
28	132.5	5.9	349	12	O57101	O57101 monkeypox v
29	132.5	5.9	349	12	O57102	O57102 monkeypox v
30	132.5	5.9	349	12	O57099	O57099 monkeypox v
31	132.5	5.9	349	12	O57291	O57291 monkeypox v
32	132	5.9	235	13	Q8JFU6	Q8jfu6 brachydanio
33	131	5.8	186	12	Q9WJB4	Q9wjb4 vaccinia vi
34	131	5.8	347	12	O57115	O57115 cowpox viru
35	131	5.8	355	12	Q85308	Q85308 cowpox viru
36	130.5	5.8	1171	11	Q8CGB2	Q8cgb2 mus musculu
37	130.5	5.8	1799	11	Q8R0Y0	Q8r0y0 mus musculu
38	130	5.8	1827	13	Q8JHV6	Q8jhv6 brachydanio
39	129	5.7	186	12	Q911R5	Q911r5 vaccinia vi
40	129	5.7	349	12	O57305	O57305 cowpox viru
41	129	5.7	848	11	Q8C720	Q8c720 mus musculu
42	129	5.7	1792	13	O57484	O57484 gallus gall
43	129	5.7	3567	11	Q9ES77	Q9es77 mus musculu
44	128.5	5.7	349	12	O57111	O57111 variola vir
45	128	5.7	507	5	Q8MS81	Q8ms81 drosophila

ALIGNMENTS

RESULT 1
Q8BUM7
ID Q8BUM7 PRELIMINARY; PRT; 416 AA.
AC Q8BUM7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK083283; BAC38842.1; -.
SQ SEQUENCE 416 AA; 45256 MW; 0DE295B591FA570A CRC64;

Query Match 69.1%; Score 1559.5; DB 11; Length 416;
Best Local Similarity 70.2%; Pred. No. 8.6e-137;
Matches 294; Conservative 36; Mismatches 84; Indels 5; Gaps 3;

```
Qy          1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
              |||||       |  :: | :|:|||:||:||||||||:||||||| | ||||||||||
Db          1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60

Qy         61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
              |||||||||||||  ||  |||||||||||||| |||:|||||:|||| ||||:|||||||
Db         61 ECGFGYGEDAQCVPCRPQRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120

Qy        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
              |||||||||||||||||||||||||||||| ||||||||:|| ||||||||||||||||||
Db        121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
```

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Qy        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
              ||||||||||||||||||||||||||||||||||||||||:|:|   ||||||  ||
Db        181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDQPRLRHCAHRACCQYHRD 240

Qy        241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
              |    ||| |:||:|||| |    | ||||: |  :|| ||     |: :| ||||:::||
Db        241 SAPMYGPVHLIPSLCCEEARSSARAVLGCGLRSPTTLQERNPASVGDTMPAFFGSVSRSI 300

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
              | ||||||||||||:|||: | ||||||||||| :|||| ||: ||||:  ||| | |
Db        301 CAEFSDAWPLMQNPLGGDS-SLCDSYPELTGEDTNSLNPENESAASLDSSGGQDLAGTA- 358

Qy        361 PVQSHSENFTAATDLSRYNN--TLVESASTQDALTMRSQLDQESGAIIHPATQTSLQEA 417
                | | : :||  |: :  |: |    |||    ||   |    :: |  |: |:|
Db        359 -ALESSGNVSESTDSPRHGDTGTVWEQTLAQDAQRTPSQGGWEDRENLNLAMPTAFQDA 416
```

RESULT 2
Q8BWR1
ID Q8BWR1 PRELIMINARY; PRT; 273 AA.
AC Q8BWR1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050262; BAC34152.1; -.
SQ SEQUENCE 273 AA; 29256 MW; B6A8E2E1F36B1769 CRC64;

Query Match 37.5%; Score 846.5; DB 11; Length 273;
Best Local Similarity 64.3%; Pred. No. 1.4e-70;
Matches 173; Conservative 26; Mismatches 65; Indels 5; Gaps 3;

```
Qy        151 SKVNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQD 210
              ||||||||:|| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 SKVNLVKISSTVSSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQD 67

Qy        211 IQYNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACSPNPATLGCG 270
              |||||||||||:|:|    |||||||  |||    ||| |:||:||||| |    | ||||
Db         68 IQYNGSELSCFDQPRLRHCAHRACCQYHRDSAPMYGPVHLIPSLCCEEARSSARAVLGCG 127

Qy        271 VHSAASLQARNAGPAGEMVPTFFGSLTQSICGEFSDAWPLMQNPMGGDNISFCDSYPELT 330
              : |  :|| ||    |: :| ||||:::||| |||||||||||:|||: | ||||||||
Db        128 LRSPTTLQERNPASVGDTMPAFFGSVSRSICAEFSDAWPLMQNPLGGDS-SLCDSYPELT 186

Qy        331 GEDIHSLNPELESSTSLDSNSSQDLVGGAVPVQSHSENFTAATDLSRYNN--TLVESAST 388
              ||| :|||| ||: ||||:  ||| | |      | | : :||  |: :  |: |
Db        187 GEDTNSLNPENESAASLDSSGGQDLAGTA--ALESSGNVSESTDSPRHGDTGTVWEQTLA 244

Qy        389 QDALTMRSQLDQESGAIIHPATQTSLQEA 417
              |||    ||   |    :: |  |: |:|
Db        245 QDAQRTPSQGGWEDRENLNLAMPTAFQDA 273
```

RESULT 3
Q8BX35
ID Q8BX35 PRELIMINARY; PRT; 297 AA.
AC Q8BX35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK049134; BAC33562.1; -.
SQ SEQUENCE 297 AA; 33066 MW; 46FEFDDC51D739BE CRC64;

Query Match 22.0%; Score 497; DB 11; Length 297;
Best Local Similarity 40.2%; Pred. No. 5.6e-38;
Matches 97; Conservative 30; Mismatches 74; Indels 40; Gaps 3;

```
Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |:||: | || | ||||| ||||:||:| | || |: |   ::|  ||  :|: |
Db          2 DCQENEYRDQWGRCVTCQQCGPGQELSKDCGYGEGGDAHCIVCPPRKYKSTWGHHRCQTC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| |||||: ||:|||||||| |||||:: | || ||:||    |  |  |  :
Db         62 ITCAVINRVQKANCTNTSNAICGDCLPRFYRKTRIGGLQDQECIPCTKQTPSSEVQCTFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQ 212
              ::|||: :    ||:  | |:: | |    || | |  :|||: |
Db        122 LSLVKVDAHTVPPREATLVALVGSLLVVFALAFLGLFFLYCKQIFNRH---------- 169

Qy        213 YNGSELSCFDRPQLHEYAHRACCQCRRDSVQ-----TCGPVRLLPSMCCEEACSPNPATL 267
                                      ||| |||:|     |     | |    :|     ||
Db        170 ----------------------CQC-RDSLQYEAEKTVEEDSLFPVPPGQETSPEFPANE 206

Qy        268 G 268
              |
Db        207 G 207
```

RESULT 4
Q8BM50
ID Q8BM50 PRELIMINARY; PRT; 297 AA.
AC Q8BM50;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK034909; BAC28879.1; -.
SQ SEQUENCE 297 AA; 33038 MW; D5F2CD188765AD65 CRC64;

Query Match 22.0%; Score 496; DB 11; Length 297;
Best Local Similarity 40.2%; Pred. No. 6.9e-38;
Matches 97; Conservative 30; Mismatches 74; Indels 40; Gaps 3;

```
Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |:||: | || | ||||| ||||:||:| | || |: |   ::|  ||  :|: |
```

```
Db          2 DCQENEYRDQWGRCVTCQQCGPGQELSKDCGYGEGGDAHCIVCPPRKYKSTWGHHRCQTC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| |||||: ||:|||||||| |||||:: | || ||:||    |  |  |  :
Db         62 ITCAVINRAQKANCTNTSNAICGDCLPRFYRKTRIGGLQDQECIPCTKQTPSSEVQCTFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQ 212
              ::|||: :    ||:  | |:: | |    || | |  :|||: |
Db        122 LSLVKVDAHTVPPREATLVALVGSLLVVFALAFLGLFFLYCKQIFNRH---------- 169

Qy        213 YNGSELSCFDRPQLHEYAHRACCQCRRDSVQ-----TCGPVRLLPSMCCEEACSPNPATL 267
                            ||| |||:|     |     | |    :|     ||
Db        170 ----------------------CQC-RDSLQYEAEKTVEEDSLFPVPPGQETSPEFPANE 206

Qy        268 G 268
              |
Db        207 G 207
```

RESULT 5
Q8IZA6
ID Q8IZA6 PRELIMINARY; PRT; 318 AA.
AC Q8IZA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE X-linked ectodermal dysplasia receptor long isoform.
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22323314; PubMed=12270937;
RA Sinha S.K., Zachariah S., Quinones H.I., Shindo M., Chaudhary P.M.;
RT "Role of TRAF3 and -6 in the Activation of the NF-kappa B and JNK
RT Pathways by X-linked Ectodermal Dysplasia Receptor.";
RL J. Biol. Chem. 277:44953-44961(2002).
DR EMBL; AY152724; AAN73210.1; -.
KW Receptor.
SQ SEQUENCE 318 AA; 34992 MW; A4C8AED32F346A3E CRC64;

Query Match 21.6%; Score 488; DB 4; Length 318;
Best Local Similarity 30.8%; Pred. No. 4.2e-37;
Matches 121; Conservative 50; Mismatches 110; Indels 112; Gaps 12;

```
Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |: |: | || | :|||| ||||:||:| | || |   |:|  ||  :|: |
Db          2 DCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQSC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| || ||:|||:|:|||||| |||||:: | || ||:||    |  |  || :
Db         62 ITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQ 212
              ::||:  :    |::  | |:: | |    || | |  :||| ||
Db        122 LSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCK-QF--------------- 165

Qy        213 YNGSELSCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVH 272
                     |:|          |:|: :       :: |        | ||:|
Db        166 --------FNR-----------HCQREKL-------IIFS-------DPVPASL----- 186

Qy        273 SAASLQARNAGPAGEMVPTPFGSLTQSICGEFSDAWPLMQNPMGGDNISFCDSYPELTGE 332
                          ::| | | | |    : :    |   |   :      |      |
Db        187 -------------NLIPEFAGGLLQFEADKTAKEESLFPVPPSKET-----SAESQVSE 227

Qy        333 DI---HSLNPELESSTSLDSNSSQDLVGGAVPVQSHSENFTAAT---------------- 373
              :|     ||| ||   |  |          | |   |:|| |:
Db        228 NIFQTQPLNPILEDDCSSTS---------GFPTQ---ESFTVASCTSESHSHWVHSPIEC 275

Qy        374 ---DLSRYNNTLVESASTQDALTMRSQLDQESG 403
                 || ::::    |||   | |:     : :|
Db        276 TELDLQKFSS----SASYTGAETLGGNTVESTG 304
```

RESULT 6
Q8BJS6
ID Q8BJS6 PRELIMINARY; PRT; 185 AA.
AC Q8BJS6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK080072; BAC37822.1; -.
SQ SEQUENCE 185 AA; 20832 MW; 7335CCAC83C829C4 CRC64;

Query Match 21.5%; Score 486; DB 11; Length 185;
Best Local Similarity 49.7%; Pred. No. 3.3e-37;
Matches 82; Conservative 28; Mismatches 55; Indels 0; Gaps 0;

```
Qy         33 DCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
              ||:: |:| : | || | ||||| ||||:||:| | || |: |   ::|  ||  :|: |
Db          2 DCQENEYRGQWGRCVTCQQCGPGQELSKDCGYGEGGDAHCIVCPPRKYKSTWGHHRCQTC 61

Qy         93 LDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASK 152
              : |||:|| ||||: ||:|||||||| |||||:: | || ||:||    |  |  |  :
Db         62 ITCAVINRVQKANCTNTSNAICGDCLPRFYRKTRIGGLQDQECIPCTKQTPSSEVQCTFQ 121

Qy        153 VNLVKIASTASSPRDTALAAVICSALATVLLALLILCVIYCKRQF 197
              ::|||: :    ||:  | |:: | |    || | |  :|||: |
Db        122 LSLVKVDAHTVPPREATLVALVGSLLVVFALAFLGLFFLYCKQIF 166
```

RESULT 7
Q9PVD4
ID Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P75-like transmembrane protein fullback.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
RT Expressed Xenopus Gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF131890; AAD54072.1; -.
DR HSSP; P07174; 1NGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.

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DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Transmembrane.
SQ   SEQUENCE   387 AA;  42066 MW;  1A386A239C7C8A82 CRC64;

  Query Match             7.6%;  Score 172;  DB 13;  Length 387;
  Best Local Similarity   23.8%;  Pred. No. 1.5e-07;
  Matches   63;  Conservative   33;  Mismatches   81;  Indels   88;  Gaps   13;

Qy         16 LLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTC 75
              ||:|:  :| :  ||||          || |  |: |  |  :   ||     | :|  |
Db         12 LLLLISKISAEDVCESG------LYTNSGKC--CSLCPAGFGVVVPCG---DSDTKCEPC 60

Qy         76 RLHRFKEDWGFQ-------KCKPCLDCAVVNRFQKANCSATSDAIC----------GDC 117
                    |:  |        ||:||  |   :   ::||:   | :|          | |
Db         61 -----IENSTFSDVRSAKAKCQPCFTCQSPSLTLESNCTREQDTVCRCPERQYLDSNGIC 115

Qy        118 LP--------------------------GFYRKTKLVGFQDMECVPC----------G 139
              ||                          ||| : |     :  |:||          |
Db        116 LPCQLCSKGHGVVSQCTHNKNTVCQLCSSGFYSEVK---SSESPCLPCRTECKETEVQIG 172

Qy        140 DPPPPYEPHCASK-VNLVK------IASTASS----PRDTA--LAAVICSALATVLLALL 186
              |  | ::  |  | | ::|        ::| |    |:| :  :  | || || |:: |:
Db        173 DCVPQHDILCMDKDVPILKRTEGGENGTSAGSPHFIPQDNSKNIIPVYCSILAAVVVGLI 232

Qy        187 ILCVIYCKRQFMEKKPSWSLRSQDI 211
                    |     :||     |: ::
Db        233 AYVAFKCYTTCKQKKQLAKARAGEL 257


RESULT 8
Q9DDD2
ID   Q9DDD2      PRELIMINARY;      PRT;   276 AA.
AC   Q9DDD2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Human CD40-homologue.
GN   TNFSF5.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tregaskes C.A.;
RL   Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR   EMBL; AJ293700; CAC20218.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00037; MYB_1; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   276 AA;  30009 MW;  4040B7E0DB82454E CRC64;

  Query Match             6.9%;  Score 155;  DB 13;  Length 276;
  Best Local Similarity   25.9%;  Pred. No. 3.7e-06;
  Matches   59;  Conservative   33;  Mismatches   72;  Indels   64;  Gaps   15;

Qy         17 LVLLG-----YLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQ 71
              | |||       | |    :: :|  ::: :  | |  ||:| || :|: ||      ||:
Db          4 LGLLGLLCALLLGCGQPGDAVNCSDKQY-EHKGRC--CNRCQPGKKLASEC--NDTEDSV 58

Qy         72 CVTCRLHRFKEDWGFQK-CKP---CLDCA--VVNRFQKA------NCSA---TSDAICGD 116
              |  |   :::  |  :: | |   | | |  :| |   |       | |    |||  |
Db         59 CTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQCRAGMHCSDASCQT 118

Qy        117 CL------PGFYRKTKLVGF--------QDMECVPCGD----------PPPPYEPHCASK 152
              |:       ||       ||           | || :           |  :   |  |
Db        119 CVENEPCKQGF-------GFVAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCEEK 171

Qy        153 VNLVKIAST------ASSPRDTALAAV--ICSALATVLLALLILCVIY 192
                 :||:  |        | | ::|: :  | :|: | |: : | |:::
Db        172 GLVVKVKGTNTSDVICESSRRSSLSVLIPITAAVVTCLVGICIYCLVH 219


RESULT 9
Q9BXI1
ID   Q9BXI1      PRELIMINARY;      PRT;  1024 AA.
AC   Q9BXI1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Nuclear transcription factor NFX2.
GN   NFX2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Li J.M., Sah J.H., Zhou Z.M.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332009; AAK16545.1; -.
DR   InterPro; IPR000967; Znf_NFX1.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF01422; zf-NF-X1; 8.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00438; ZnF_NFX; 9.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE   1024 AA;  113623 MW;  4228E14EEF42E3BC CRC64;

  Query Match             6.4%;  Score 145;  DB 4;  Length 1024;
  Best Local Similarity   18.5%;  Pred. No. 0.00016;
  Matches  110;  Conservative   61;  Mismatches  188;  Indels  236;  Gaps   27;

Qy         24 SCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG-------FGYGEDAQC---- 72
              || : |  |                 ||  |   |  : |||       |     |
Db        456 SCNLLCHPG--------------PCPPCPAFMTKTCECGRTRHTVRCGQAVSVHCSNPC 500

Qy         73 ---VTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATS-DAICGDCLPGFYRKTKLV 128
                 : |  |:  |     :|:||    ::|  |   | :|| | :||  :       |
Db        501 ENILNCGQHQCAELCHGGQCQPCQ--IILN--QVCYCGSTSRDVLCGTDV------GKSD 550

Qy        129 GFQDMEC-------VPCGD--------PPP-------PYEPHC--ASKVNLVKIASTASS 164
              || |  |        : ||:         | |       |     |    :  | ::    ||
Db        551 GFGDFSCLKICGKDLKCGNHTCSQVCHPQPCQQCPRLPQLVRCCPCGQTPLSQLLELGSS 610

Qy        165 PRDTALAAV-----IC-SALATVLLALLILC----------------VIYCKRQFMEKK- 201
              | | :  |     :|   |    |  :  |                  || |:  |  |:
Db        611 SRKTCMDPVPSCGKVCGKPLPCGSLDFIHTCEKLCHEGDCGPCSRTSVISCRCSFRTKEL 670

Qy        202 PSWSLRSQDI--------------QYNGSELSCFDRPQ-------------LH---EYA 230
              |  ||:|:|                  ::  :|: | |:                ||   |
Db        671 PCTSLKSEDATFMCDKRCNKKRLCGRHKCNEICCVDKEHKCPLICGRKLRCGLHRCEEPC 730

Qy        231 HRACCQ-CRRDSVQT----CGPVRLLPSMCC--------------------------EE 258
              ||  || | : |       ||   : | : |                          ||
Db        731 HRGNCQTCWQASFDELTCHCGASVIYPPVPCGTRPPECTQTCARVHECDHPVYHSCHSEE 790

Qy        259 ACS-----------------------------PNPATLGCGVHSAASL---------- 277
              |                             |  ||| ||:|    |
Db        791 KCPPCTFLTQKWCMGKHEFRSNIPCHLVDISCGLPCSATLPCGMHKCQRLCHKGECLVDE 850

Qy        278 -------------------------------QAR-----NAGPAGEMVPTFFGSLTQSI 300
                                            :|:      |   |||     | |
Db        851 PCKQPCTTPRADCGHPCMAPCHTSSPCPVTACKAKVELQCECGRRKEMVICSEASSTYQR 910

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
                  | |  :   :||     :   :| :::|    | :   |     :  :  |
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Db        911 IAAISMASKITDMQLGGS----VEISKLITKKEVHQARLECDEECSALERKKR--LAEAF 964

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQ 415
Db        965 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLVEAVNKVEVE 1017


RESULT 10
Q96EL5
ID   Q96EL5      PRELIMINARY;      PRT;  1120 AA.
AC   Q96EL5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; BC012151; AAH12151.1; -.
DR   InterPro; IPR001374; R3H.
DR   InterPro; IPR006895; zf-Sec23_Sec24.
DR   InterPro; IPR000967; Znf_NFX1.
DR   InterPro; IPR001965; Znf_PHD.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF01424; R3H; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF01422; zf-NF-X1; 8.
DR   Pfam; PF04810; zf-Sec23_Sec24; 1.
DR   SMART; SM00393; R3H; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00438; ZnF_NFX; 9.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   1120 AA;  124394 MW;  F2203BE1DB6437E6 CRC64;

  Query Match             6.3%;  Score 142;  DB 4;  Length 1120;
  Best Local Similarity   18.8%;  Pred. No. 0.00035;
  Matches  110;  Conservative   58;  Mismatches  182;  Indels  236;  Gaps   27;

Qy         24 SCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECG-------FGYGEDAQC---- 72
Db        456 SCNLLCHPG--------------PCPPCPAFMTKTCECGRTRHTVRCGQAVSVHCSNPC 500

Qy         73 ---VTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATS-DAICGDCLPGFYRKTKLV 128
Db        501 ENILNCGQHQCAELCHGGQCQPCQ--IILN--QVCYCGSTSRDVLCGTDV------GKSD 550

Qy        129 GFQDMEC-------VPCGD--------PPP-------PYEPHC--ASKVNLVKIASTASS 164
Db        551 GFGDFSCLKICGKDLKCGNHTCSQVCHPQPCQQCPRLPQLVRCCPCGQTPLSQLLELGSS 610

Qy        165 PRDTALAAV-----IC-SALATVLLALLILC----------------VIYCKRQFMEKK- 201
Db        611 SRKTCMDPVPSCGKVCGKPLPCGSLDFIHTCEKLCHEGDCGPCSRTSVISCRCSFRTKEL 670

Qy        202 PSWSLRSQDI---------------QYNGSELSCFDRPQ-------------LH---EYA 230
Db        671 PCTSLKSEDATFMCDKRCNKKRLCGRHKCNEICCVDKEHKCPLICGRKLRCGLHRCEEPC 730

Qy        231 HRACCQ-CRRDSVQT----CGPVRLLPSMCC--------------------------EE 258
Db        731 HRGNCQTCWQASFDELTCHCGASVIYPPVPCGTRPPECTQTCARVHECDHPVYHSCHSEE 790

Qy        259 ACS-----------------------------PNPATLGCGVHSAASL---------- 277
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Db        791 KCPPCTFLTQKWCMGKHEFRSNIPCHLVDISCGLPCSATLPCGMHKCQRLCHKGECLVDE 850

Qy        278 --------------------------------QAR-----NAGPAGEMVPTFFGSLTQSI 300
Db        851 PCKQPCTTPRADCGHPCMAPCHTSSPCPVTACKAKVELQCECGRRKEMVICSEASSTYQR 910

Qy        301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Db        911 IAAISMASKITDMQLGGS----VEISKLITKKEVHQARLECDEECSALERKKR--LAEAF 964

Qy        361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAII 406
Db        965 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 1008


RESULT 11
Q8BTV0
ID   Q8BTV0      PRELIMINARY;      PRT;   436 AA.
AC   Q8BTV0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 19-like
DE   homolog.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK088621; BAC40459.1; -.
SQ   SEQUENCE   436 AA;  46518 MW;  E61304480DBA0815 CRC64;

  Query Match             6.2%;  Score 141;  DB 11;  Length 436;
  Best Local Similarity   22.0%;  Pred. No. 0.00013;
  Matches   71;  Conservative   33;  Mismatches  103;  Indels  116;  Gaps   15;

Qy         52 CGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSD 111
Db         39 CPPGKEPDPDPGQG----TLCRTCPPGTFSASWNSYPCQPHYRCSLQKRLEAQAGTATHD 94

Qy        112 AICGDCLPGFYRKTKLVGFQDMECVPCGDPPP--------------------------P 144
Db         95 TMCGDCQHGWFGPQ---GVPHVPCQPCSKAPPSTGGCDESGRRGRRGVEVAAGTSSNGEP 151

Qy        145 YEPHCASKVNLVKIASTASSPRDTALA-AVICSALATVLLALL--ILCVI------YCKR 195
Db        152 RQPGNGTR---------AGGPEETAAQYAVIAIVPVFCLMGLLGILVCNLLKRKGYHCTA 202

Qy        196 QFMEKKPS---------WSLRSQDI---------------QYNGSE----LSCFDRPQLH 227
Db        203 Q-KEVGPSPGGGGSGINPAYRTEDANEDTIGVLVRLITEKKENAAALEELLKEYHSKQLV 261

Qy        228 EYAHRACCQCRRDSVQTCGPV-RLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAG 286
Db        262 QTSHR--------------PVPRLLPA-------SPSIPHICPHHHHLHTVQG------- 293

Qy        287 EMVPTFFGSLTQSICGEFSDAWP 309
Db        294 ------LASLSGPCCSRCSQKWP 310


RESULT 12
Q9GQ45
ID   Q9GQ45      PRELIMINARY;      PRT;   548 AA.
AC   Q9GQ45;
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DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Variant-specific surface protein M21-1 (Fragment).
GN   M21-1.
OS   Giardia lamblia (Giardia intestinalis).
OC   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX   NCBI_TaxID=5741;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ad-1;
RA   Mansouri M., Ey P.L.;
RT   "A segment of a vsp72-like gene homolog from a type A-I (group 1)
RT   Giardia intestinalis isolate.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF298862; AAG37862.1; -.
DR   HSSP; P00136; 2CY3.
DR   InterPro; IPR006058; 2Fe2S_ferredoxin.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR002350; kazal.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00261; FU; 3.
DR   PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS00282; KAZAL; 1.
FT   NON_TER       1      1
FT   NON_TER     548    548
SQ   SEQUENCE   548 AA;  56557 MW;  578FE4FDA0A2CF0E CRC64;

  Query Match             6.2%;  Score 140.5;  DB 5;  Length 548;
  Best Local Similarity   24.3%;  Pred. No. 0.0002;
  Matches   69;  Conservative   22;  Mismatches  124;  Indels   69;  Gaps   16;

Qy          21 GYLSCK-----VTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVTC 75
               | : |       |||  |          ::  ||   ||  |        |       ||  |
Db         182 GCIDCTGANQCTTCEDGKYL------KNNQCVDAGQCDQGTYADPTTG-------QCKPC 228

Qy          76 RLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAI----------C---GDCLPGFY 122
                     |   |  |   | :::  |   || :|: :           |   | |  |
Db         229 ---------GITDCATCEYNATISQPQCKTCSTSSNKMVKTAADGTTTCVDDGGCTNG-- 277

Qy         123 RKTKLV-GFQDMECVPCGDPPPPYE---PHCASKVNLVKIASTASSPRDTALAAVICSAL 178
                 |  | |     ||||||          |:||    |        |:    | |:|
Db         278 -NTHFVEGTNQKLCVPCGDTTNGGVLGCNTCSSKTTCTK---CLDGYYDSGSGTVTCTAC 333

Qy         179 ATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCR 238
                  |   ||  | |||    || : |:      :|  :|| |:   :   |  |  |
Db         334 PGANCA--TLCERY-KRQCTTCKPGFFLKDSS---SGECISCSDK---NNGGHEGCSACS 384

Qy         239 RDSVQTCGPVR-------LLPSMCCEEACSPNPATLGCGVHSAA 275
                :    |   :          :  | : |    |   ||  | |
Db         385 SNGAFKCTDCKPNYKKEGTSDNYTCVKTCEDETA---CGGTSGA 425


RESULT 13
Q8JFV6
ID   Q8JFV6      PRELIMINARY;      PRT;   317 AA.
AC   Q8JFV6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   SI:dZ107D16.1 (Novel protein similar to vertebrate nerve growth factor
DE   receptor (NGFR)) (Fragment).
GN   SI:DZ107D16.1.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ramsay H.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL591671; CAD43421.1; -.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
FT   NON_TER       1      1
FT   NON_TER     317    317
SQ   SEQUENCE   317 AA;  34446 MW;  D9B7EF1C70DAF92B CRC64;

  Query Match             6.2%;  Score 139;  DB 13;  Length 317;
  Best Local Similarity   22.7%;  Pred. No. 0.00014;
  Matches   58;  Conservative   25;  Mismatches  113;  Indels   60;  Gaps   11;

Qy          21 GYLSCKVTC-ESGD----CRQQEFRD-RSGNCVPCNQCGPGMELSKECGFGYGEDAQCVT 74
               | :  :  | :| |     |    | :  |  | ||  |  |  :    |   :  | |
Db          76 GLMRMQTPCTDSNDAECVCNYGYFMNVLSSRCEPCTVCPLGQGVDMRCELNH--DTVCEE 133

Qy          75 CRLHRFKEDWG-FQKCKPCLDCAVVNRFQKANCSATSDAICGDCL-PGFYRKTKLVGFQD 132
               ||   : :       | ||  |          ||: | ||:| | | | :   |   |  |
Db         134 CRDETYSDQENTMDPCMPCTICEEDTEILLRNCTPTEDALCHDPLSPTYPTSTGDSGSFD 193

Qy         133 MECVPCGDP--------PPPYEPHCASK---VNLVKIASTASSPRDTALAAVICSALATV 181
                 :       |        | |  ||    :    ||: |                || || |
Db         194 TDLDRLWSPSPGDDATTPKPSSPHFIGRGLNENLIPI--------------YCSILAAV 238

Qy         182 LLALLILCVI----YCKR-------------------QFMEKKPSWSLRSQDIQYNGSE 217
               :: ||   :      ||:                  : :      |: || :|   ::
Db         239 VVGLLAYIIFKRWNSCKQNKQAANNRAATANQTPSPEGEKLHSDSGISVDSQSLQEQQAQ 298

Qy         218 LSCFDRPQLHEYAHRA 233
                     : | |   | |
Db         299 TQTQAQAQAHTQLHAA 314


RESULT 14
O72735
ID   O72735      PRELIMINARY;      PRT;   186 AA.
AC   O72735;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   A53R protein.
GN   A53R.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "Species-specific differences in genome organization of cowpox,
RT   smallpox, and vaccinia viruses.";
RL   Virology 243:432-460(1998).
DR   EMBL; Y15035; CAA75273.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   186 AA;  20482 MW;  D2342F1040A00AE3 CRC64;

  Query Match             6.1%;  Score 138.5;  DB 12;  Length 186;
  Best Local Similarity   28.0%;  Pred. No. 7.8e-05;
  Matches   46;  Conservative   19;  Mismatches   68;  Indels   31;  Gaps   11;
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Qy          11 KTFFTLLVLLGYLSCKVTCE----------SGDCRQQEFRDRSGN-CVPCNQCGPGMEL 58
               |:   :  :| |::  || :           :| | : |: |:  | |  |||| ||
Db           4 KSLLAVCTIL-YITTLVTADIPTPLPPHAPVNGSCDEGEYLDKRHNQC--CNQCPPGEFA 60

Qy          59 SKECGFGYGED-AQCVTCRLHRFKEDWGFQK-CKPCLDCAVVNRFQKANCSATSDAICGD 116
                  |    | |  :|  |  | :     :   |  |  |     | |  |: | :: |
Db          61 KVRCS---GSDNTKCERCPPHTYTAIPNYSNGCHQCRKCP-TGSFDKVKCTGTQNSKC-S 115

Qy         117 CLPGFYRKTKLVGFQD-MECVPCGDPPPPY--------EPHCAS 151
               ||||:|  |     :|  :|||    |  |         | | |
Db         116 CLPGWYCATDSSQTEDCRDCVPKSRCPCGYFGGIDEQGNPICKS 159


RESULT 15
O57123
ID   O57123      PRELIMINARY;      PRT;   350 AA.
AC   O57123;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Munich OPV90/5(cat);
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90235; AAB94391.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   350 AA;  38113 MW;  CC3291D8554E4F74 CRC64;

  Query Match             6.1%;  Score 136.5;  DB 12;  Length 350;
  Best Local Similarity   26.9%;  Pred. No. 0.00027;
  Matches   43;  Conservative   19;  Mismatches   61;  Indels   37;  Gaps    8;

Qy          11 KTFFTLLVLLGYLSCKVTCES--------GDCRQQEFRDRSGNCVPCNQCGPGMELSKEC 62
               |::  || ||  ||| :   |         | |:  |:|.     : |  | ||    |: |
Db           2 KSYILLLPLL--LSCIIIINSDITHEPSNGKCKDNEYRHHH---LCCLSCPPGTYASRLC 56

Qy          63 GFGYGEDAQCVTCRLHRF-KEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPGF 121
                  : ||  |    |   :     |  |      |: :  :|: | : || || ||:
Db          57 DSKTNTNTQCTPCGSDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRIC-DCAPGY 115

Qy         122 Y-------------RKTKL-VGF--------QDMECVPCG 139
               |              :||  :|:         |: | |||
Db         116 YCLLKGSSGCKACISQTKCGIGYGVSGHTSAGDVVCSPCG 155


Search completed: January 29, 2004, 21:40:00
Job time : 42 secs
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